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AF149721 Homo sapi
AF129721 Homo sapi
AF181850 Homo sapi
AF177756 Mus muscu
AF177755 Mus muscu
AC114608 Mus muscu
AC124475 Mus muscu
AC12534 Rattus no
AC125534 Rattus no
AR135534 Romo sapi
AF149722 Homo sapi
AX147722 Homo sapi
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AF062748 Homo sapi
AC107214 Homo sapi
AC107236 Mus muscu
AC122966 Rattus no
AC128348 Rattus no
AC129658 Rattus no
AC124017 Xenopus 1
AC144762 Homo sapi
AB098919 Bos tauru
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AR154563 Sequence
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AR213555 Sequence
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1 MLGQQQQLYSSAALLTGER.....DNEKTMDKSTEKTKKDRRSR
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                      nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Sequence Homo sapi

Sequence

Sequence Homo sapi Sequence

Homo sapi

QY         221         SerTyrGlyGluMetIleGlyCygAspAsnGluGlnCysProlleGluTrpPheHisPhe 240           Db         661         TCTTATGGGAGATGATAGGATGTGACAATGAACGATGTCCAATTGAATGCTTTCACTTT         720           QY         241         SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly         260           QY         261         AspAsnGluLysTracctaTaAaCcAaAgGGGAAATGGTATTGCCCAAAGTGCAGGGA         780           QY         261         AspAsnGluLysTrMetAspLysSerThrGluLysThrLysLysBapArgargSerArg         280           Db         781         GATAATGAGAAAACAATGGACAAAAGGACAAAAAGGATAGAGATGGAGG         80           RESULT 2         AR213555         AR213555         LOCUS           DNA         11nnear         PAT 25-SEP-2002           ACCESSION         AR213555         GI:23310822	SOURCE Unknown.  ORGANISM Unclassified.  ORGANISM Unclassified.  REFERENCE 1 (bases 1 to 1078)  AUTHORS Nagata,M., Ozaki,K., Shimada,Y. and Horie,M.  TITLE 1solated DNA molecule encoding human TSC403  JOURNAL Patent: US 6403785-A 7 11-JUN-2002;  FEATURES 1.010/94011fiers  SOURCE 1.010/94011fiers  ACCOUNT 356 a 206 c 280 g 236 t	Scores: 1.92e-113 1481.00 milarity: 100.00\$ Similarity: 100.00\$ h: 6	US-09-513-365A-1 (1-280) × AR213555 (1-1078)  QY	Oy 41 AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu 60	332 CGTCTACAGCAGTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAA  101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgGlaArTGGAGATGAAAA  101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgGlaArGGLULeu  392 ATACAGATTGTTACAAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAATGGAGTTA  121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet  122 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet  123 HisSerGlnCysPheGluArgSerSerArgArgArgGraCCTCAGATAAGCAAGATG  141 AspSerSerGlnProGluArgSerSerArgArgArgProArgArgGlnArgThrSerGluSer  141 AspSerSerGlnProGluArgSerSerArgArgArgProArgArgGlnArgThrSerGluSer  152 GATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAGGGGGGGG
AR213554	Alignment Scores: Pred. No.: Pred. No.: Score: Score: 1.39e-113 Length: 840 Score: 1481.00 Matches: 280 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 DB: 6 Gaps: 0 US-09-513-365A-1 (1-280) x AR213554 (1-840) QY 1 MetLeuGlyGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg 20	Db   1	Qy         61 LysGlulleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys 80           Db         181 AAGGAAATTGATGATGTCTACGAAAATATAAGAAGAGATGATTTAAACCAGAAGAAA 240           Qy         81 AxgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100           Db         241 CGTCTACAGCAGCTTCTCCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAA 300           Oy         101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgAlaArgGluMetGluLeu 120		00   00   00   00   00   00   00   0

QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD RRSR" RRSR" 356 a 206 c 280 g 236 t ORIGIN	Alignment Scores:  Pred. No.: Pred. No.: Score: Score: 1.92e-113 Length: 1078  Score: 1481.00 Marches: Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 100.00\$ Indels: 0 BB:		Db 92 ATGTTAGGGCAGCAGCAGCAGCATGTACTCGTCGGCCGCGCTCCTGACCGGGGAGCGG 151  Qy 21 SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis 40		212 GACATGCAGAGAACGTGTCTGTGCTGCGAGAGCTGGACAACAAATATCAAGAAACGTTA	Qy 61 LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGluLysLys 80 	Qy 81 ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100 	Oy 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAenargAlaArgGlnMetGluLeu 120 	Oy 121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet 140	Qy 141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSer 160	Qy         161 ArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspAspGlnProProLysGlu 180           Db         572 CGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCATCACCACCTAAAGAA 631	Qy       181 LyslysSerlysSerAlaLysLysLysLysEysArgSerlysAlaLysGlnGluArgGluAla       200	Qy         201 SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal 220	Qy 221 SerTyrGlyGluMet1leGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240	Qy         241         SerCysValSerLeuThrTyrLysBroLysGlyLysTrpTyrCysProLysCysArgGly         260		Db 872 GATAATGAGAAAACAATGGACAAAAGTACTGAAAAGGAAAAAAGGATAGAAGGTGGGG 931 RESULT 4 AX211560
Oy 161 ArgAspLeuCysHisMetAlaAsnGlylleGluAspCysAspAspGlnProProLysGlu 180 	Qy         181 LysbysSerLysSerAlaLysLysLysLysAgeReLysAlaLysGluArgGluAla         200           bb         632 AAGAAATCCAAGGCAAGAAAAAAAAGAAACGCTCCAAGGCCAAGGCAAGGAAGG	Oy 221 SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe 240	Qy         241 SerCysValSerLeuThrTyrLysBroLysGlyLysTrpTyrCysBroLysCysArgGly 260           Db         812 TCATGTGTTTCACTTACCTATAAACCAAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGA 871	Oy 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg 280 	SULT 3	LOCUS DEFINITION Homo sapiens INGIL mRNA for INGILD, complete cds. ACCESSION AB012893 CT. ACCESSION AD012863	S INCLED. Homo sapiens (human) Homo sapiens	ENKATYOCA: MECAZOA: CHOYGACA; CYANIACA; Vertebraca; Euteleostomi;  REFERENCE 1 (sites) AUTHORS Shimmeda,Y., Suzuki,M., Takahashi,E. and Horie,M.  TITTE Closing of a nowell case (twitt) homelogues.	AL Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998) NE 99172097	Shimada,Y., Saito,A. and Horie,M.	JOURNAL SUBMISSED (1974) JOHN 1989 Yoshikazu Shimada, Otsuka Pharmaceutical Co. Ltd., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho, Tokushima, Tokushima 771-0192, dapa. (E-mail:shimootsuka.genome.ad.jp, Tel:81-886-65-2888 (ex.2476),	equence u	/ Organism="homo sapiens" /mol_type="manN," /db_xref="taxon:9606" /chromosome="4"	/map="4q35.1" /dev_stage="fetal" /disue_lib="fetal-brain" gene /078	CDS 92934 /gene="MKGIL" /codon start=1	/product="INGILp" /protein_id=BRA3619.1" /h vref="G1.411eces"	/ LTAINS A TO IN THE WILD OVER THE TO THE WORK TO THE TO THE WORK TO THE TO THE WORK THE WORL THE TO THE WORL THE WORL THE TO THE WORL THE WOR

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RRSR"
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                                                                                                                               SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly 260
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1080)
                                                                                  668 TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
                                                                                                                                                                                                                GATAATGAGAAAACAATGGACAAAAAGTACTGAAAAAAGACAAAAAAGGATAGAAGATCGAGG
                                                                SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPhe
    SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P., Pedeux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53 Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001) 21396501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                To (bases 1 to 1080)
Nagashima,M., Hagiwara,K., Minter,A.R. and Harris,C.C.
Direct Submission
Submitted (12-MAR-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Drive Bldg.37 Rm.2C01,
Bethesda, MD 20892, USA
Location/Qualifiers
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Matches:
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                                                                                                                                              Harris, C.C. and Nagashima, M.
Harris, C.C. and Nagashima, M.
Tumour suppressor gene, p47ing3
Patent: WO 0159114 A 7 16-AUG-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
Location/Qualifiers
                                                                               Homo sapiens (human)
Homo sapiens
Eukaryota, Metacos; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
Mismatches:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  REFERENCE AUTHORS Strausberg, R. TITLE Direct Submission JOURNAL Centect Submission Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail nih.gov Tissue Procurement: DCTD/DTP CDNA Library Preparation: Rubin Laboratory CDNA Library Preparation: Rubin Laboratory CDNA Library Prayeration: Rubin Laboratory CONTACT: Maryland; Maryland; Web site: http://www.nisc.nih.gov Acontact: nisc mgcenhogi.nih.gov Acontact: nisc mgcenhogi.nih.gov Akhter,N., Ayelle,K., Beckfrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,V., Haghighi,P., Hansen,N., Ho,SL., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., Pearsenon,R., Stantrippop,S., Thomas,P.J., Touchen,J.W., Taurgeon,C., Vort J. L. Walker, M. & Warhach,W. R. D., Touchen,J.W., Taurgeon,C., Vort J. L. Walker, M. & Warhach, W. D., Gronen,J.W., Taurgeon,C., Vort J. L. Walker, M. & Warhach, W. D., Touchen,J.W., Taurgeon,C., Vort J. L. Walker, M. & Warhach, W. D., Touchen,J.W., Taurgeon,C., Vort J. L. Walker, M. & Walker, W.	Clone distribution. MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAL Plate: 15 Row: m Column: 11  This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504694.  FEATURES  1. 1144  Source  //organism="Homo sapiens" //ml_rype="mRNA" //ml_rype="mRNA" //ml_rype="mRNA" //ml_rype="mRNA" //ml_rype="mRNA" //ml_rype="mRNA" //ml_rype="mRNA" //ml_rype="mRNA"	/ Clone="MGC:10524 IMAGE:3941655" / clone="MGC:10524 IMAGE:3941655" / tissue type="Lung, small cell carcinoma" / clone="Lib="NAH MGC 7" / lab host="DH10B="R" / note="Vector: pOTB7" / lab host="DH10B="R" / codon state="Codon st	### BASE COUNT 373 a 221 c 302 g 245 t  ORIGIN  Alignment Scores: Pred. No.: Score: Score: 100.00* Best Local Similarity: 100.00* Mismatches: 0 Query Match: 9 US-09-513-365A-1 (1-280) x BC030128 (1-1141)  Qy
Best Local Similarity: 100.00%   Mismatches: 0   Ouery Match: 100.00%   Indels: 0   Gaps: 0   Ouery Match: 9   Gaps: 0   Ouery Match: 9   Ouery Match: 9   Ouery Match: 9   Ouery Match: 9   Ouery Match: 100.00%   Ouery Match: 0   Ouery Match: 1-280)   x AF053537 (1-1080)   Ouery Match: 0   Oue	Qy         101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgalaArgGlnMetGluLeu 120           Db         368 ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGAATGGAGTTA 427           Qy         121 HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLySAlaLySMet 140           Db         428 CACTCACAGTTTCCAAGATCTTGTAAGTGAAGACCCAGATAAAGCAAAGATG 487           Qy         141 AspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgArsGCluSer 160           Db         488 GATTCCAGCCAACAGAAAGATCTTCAAGAAGACCCCGCAGGCAG	181 LyslysSerlysSerlallysLyslysBySerlysBalaysIIII	"." 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgGcGAAATGGTATTGCCCAAAGTGCAGGGAA  "." 261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg  # AspAsnGaAAACAAAGCAAAAGTACTGAAAGGATATGCCCAAAGTGCAGG  # AspAsnGaAAACAAAGGACAAAAGTACTGAAAAGAAAAAAAAAAAA

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QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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Matches:
Conservative:
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Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys
                                                                                                                                                  ArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys
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Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo. Facultad de Medicina., C/ J
Claveria s/n., 33066, SPAIN
Location/Qualifiers
                                           SerValLeuArgGluLeuAspAsnLysTyrGl
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ING2,a new possible gene supressor tumor
Unpublished
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Homo sapiens mRNA for p32
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                                           AspMetGlnArgAsnVal
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/tränslation="MLGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQ RNVSYLRELDNKYQETLKEIDDYYEKYKENDSNGKKRLOGHLQRALINSGELGDEKI QIYTQMLELVENRARQMELHSGCFQDPAESERASDKSKMDSSQPERSSRRPRRQRTSE SRDLCHMTNGIDDCDDQPPKERRSKAKKKRSKAKQERBASPVEFAIDPNEPTYCLC NQVSYGEMIGGDNEQCPIEWPHFSCVSLTYKPKGKWYCPKCRGDDNEXTMDKSTEKTKK
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          'product="Similar to inhibitor of growth family, member
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Mismatches:
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Matches:
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                                               /protein_id="AAH50003.1"
/db_xref="GI:29436710"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963706. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter_N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupte,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskiri,B., Mastrian,S.D.,McCloskey,J.C.,
McClowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 1262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
SerCysValSerLeuThrTyrLysBroLysGlyLysTrpTyrCysProLysCysArgGly
                                                                                                                                                                   AspasnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg
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                                                                                       TCTTATGGGGGAGATGATGATGATGAATGAATGAACAGTGTCCAATTGAATGGTTTCACTTT
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Email: cgapbs-remail.nih.gov
Tissue Prcourement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                           BC050003 1262 bp mRNA li
Mus musculus, Similar to inhibitor of growth
clone IMAGE:6515125, mRNA, partial cds.
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old mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam2"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/clone="IMAGE:6515125"
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/strain="FVB/N-3"
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BC050003.1 GI:29436709
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                                                                                                           LeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLys
                                                                                                                                                                                                                       428 ATGGATTCCAGTCAACCGGAAAGATCTTCTAGAAGACCTCGAAGACAGAGACCAGTGAG
                                                                                                                                                                                                                                                                          488 AGCCGTGACTTATGTCACATGACAAACGGGATTGACGACTGTGATGATGATCAACCACCGAAA
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Jones, K.A., Volkmuth, W. and Walker, M.G.
Bone remodeling genes
Patent: US 6426186-A 81 30-JUL-2002;
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In Ragashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.

Direct Submission

Submitted (16-JUL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37

Convent Dr., Bldg, 37, Rm. 2C01, Bethesda, MD 20892, USA

1. coation/Qualifiers

1. 1001

Amol_type="mRNA"

Amol_type=
   1145 TTTTCATGTGTTTTCACTCACCTATAAACCCCAAGGGGAAATGGTATTGCCCAAAGTGTAGG 1204
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                   MetLeuGly---GinGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGlu
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YYQYLLELDRRARQMELHSQCFQDASEBRASDRARDSQPBRSSRSTBES
RDLCHWANGIEDCDDQPPKBKKSKARKKKRSKAKQBREASPVEFAIDPNEFYCLCN
QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MLGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQF"
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                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                              Human Carcinogenesis,
Dr. Bldg.37, Rm.2C26,
                                                                                               Nagashima, M. Hagiwara, K., Minter, A.R. and Harris, C.C. Direct Submission
Submitted (01-MAY-1998) Laboratory of Human Carcinogen
National Cancer Institute, 37 Convent Dr. Bldg.37, Rm. Bethesda, MD 20892, USA
Location/Qualifiers
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join(AF062747.1:68. .239,124. .794)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
order(AF062247.1:1. .423,1.
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/gene="ING2"
/number=2
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/gene="ING2"
/evidence=experimental
/evidence=255 g 26
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/protein_id="AAG11396.1"
/db_xref="G1:9992842"
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AF062748
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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  St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51-18. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                             Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Sep 20, 2002 this sequence version replaced gi:20128734.
                                                                                                              Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There is an unresolved tandem repeat from base 87660 to 89441.
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                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center
Center code: WUGSC
University School of Medicine, 4444 Forest Park Parkway,
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Location/Qualifiers
1. .183317
                                                                                                                 Genetics,
                                                                                                                                      St. Louis,
                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                              Department of Park Avenue, S
                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: H_NH0367N14
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/db_xref="taxon:9606"
/chromosome="4"
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66. .840
/rpt_family="L1"
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2782. .3112
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/rpt_family="MaLR"
                                                                                                                                 University, 4444 Forest 7 (bases 1 to 183317)
                                                                                         Direct Submission
Submitted (03-OCT-2002)
                     MO 63108, USA
6 (bases 1 to 183317)
Waterston, R.
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Homo sapiens BAC clone RP11-367N14 from 4, complete sequence.
AC107214
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Catarrhini; Hominidae; Homo.
                         285 GAAAATCGGGCAAGACAAATGGAGTTACACACTCACAGTGTTTCCAAGATCCTGCTGAAAGT
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  GluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSer
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licine, 4444 Forest Park Parkway, St.
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Submitted (20-SEP-2002) Genome Sequencing Center, Washington
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Nguyen,C., Haglund,K. and Spalding,L.
The sequence of Homo sapiens BAC clone RP11-367N14
Upublished (2001)
3 (bases 1 to 183317)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Mammalla, Eutheria, Primates;
1 (Dases 1 to 18317)
Sulston, J.E. and Waterston, R.
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Waterston, R.H.
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Homo sapiens
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Direct Submission
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Submitted (07-MAR-2003) Whitehead Institute/MIT Center for Genome
                            NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemietry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 191671 bases at least Q40
Consensus quality: 192003 bases at least Q20
Consensus quality: 192003 bases at least Q20
Insert size: 188000; agarose-fp
Insert size: 188000; agarose-fp
Insert size: 181000; agarose-fp
Quality coverage: 9.1 in Q20 bases; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: 119778
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Submitted (17-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Si (bases 1 to 192753)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Cook, A., Cook, P., Corum, B., Darachlano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., FritzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Plerre, N., Hagopian, D., Hagopian, D., Hagos, B., Hall, J., Horne, R., Liu, G., Lui, R., Madopiat, D., Hagos, B., Maclean, C., Lindblad-Toh, K., Liu, G., Lui, A., Mathews, C., McCarthy, M., Maddonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Madorim, J., Meneus, L., Mihowa, T., Matthews, C., McCarthy, M., Maclon, R., Liu, G., Lui, M., Matthews, C., McCarthy, W., Maclon, J., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raywond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Steamge-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Winner, Suhmission
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                                                                              AC107236 192753 bp DNA linear HTG 07-MAR-2003
Mus musculus clone RP23-296C23, WORKING DRAFT SEQUENCE, 7 unordered
                                       252 LysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThrGlu 271
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 192753)
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Millen,C., Marie, Merzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,H., Alsbrooks,S., Anin,A., Angulano,D., Anyalebochi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baladen,D., Bandaranalke,D., Barber,M., Barneted,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Baldorin,D., Bandaranalke,D., Barber,M., Barneted,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Calderon,E., Cardenas,V., Cher,Z., Chu,J., Chacco,J., Chavez,D., Chang,C.C., Ding,Y., Calderon,E., Dederich,D., Denson,S., Deramo,C., Ding,Y., Dinh,H., Daya,R.K., Garla,M., Hamilton,K., Hanilton,K., Manillia,M., Mahilla,M., Marilla,M., Mahilla,M., Marilla,M., Maril
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Baylor Plaza, Houston, TX 77030, USA.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the serimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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Direct Submission
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Rat Genome Sequencing Consortium.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
Rattus.
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                                                                                                                                                                                                                                                                                        TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp :::
                                                                                                                                                                                                                                                                                                                                     98076 TITITAGAAACGITAAAGGAAATIGAIGAIGICTATGAAAAATATAAGAAAAAGAIGAI
                                                                                                                                                                                                                                                                                                                                                                                     LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                     98016 TCCAACCAGAAAAACGCCTACAGCAGCATCCCCAGAGAGCGTTAATCAATAGCCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97956 TIGGGAGATGAAAAATTCAGATTGTCACCCAGATGCTCGAATTGGTGGAGAAACCGAGCG
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_FULTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                       9.21e-84
1157.00
98.22*
95.56*
                                                                                                                 Percent Similarity:
Best Local Similarity:
                                               Alignment Scores:
Pred. No.:
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Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyaleberdi, V., Aoyagi, A., Ayodi, M., Baca, B., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J.,
Davila, M.L., Davis, C., Davy-Carroll, E., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Farnandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gabisi, A., Gabre, R., Garra, M., Guevara, W.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACL28348 245104 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-129P3, WORKING DRAFT SEQUENCE, 3
unordered pieces.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                        53176 TTGGGAGATGAAAAGATTCAGATTGTCACACAGATGCTGGAATTGGTGGAAAACCGAGCC
                                                                                                                                                                    156 ArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAsp
                                                                                                                                                                                                                                                                                                                               196 GlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCys
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                                                               LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla
                                                                                                                                              ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSer
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AC128348.3 GI:25007900
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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AC128348/c
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contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                   TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp :::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 225634: contig of 225634 bp in length 225635 225734: gap of unknown length 225735 231311: contig of 5577 bp in length. Location/Qualifiers 1. 231311
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                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Matches:
Conservative:
Mismatches:
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-210B24"
3446. .102459
/note="clone_boundary
                                                                                                    Center: Baylor College of Medicine
Center code: BCM
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complement(218103. .218757)
/note="clone_boundary
clone_end:Sp6
site:
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clone_end:Sp6"
49448 c 50231 g 60699
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clone_end:Sp6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end_sequence:BH343918"
                                                                                        ----- Genome Center
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1152.00
98.22$
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvardez, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harnandez, J., Harnandez, S., Hladun, S.L., Hodgson, M., Hogues, M., Howells, S., Hilay, S., Hume, J., Idlebird, D., Jackson, L., Jacob, L., Jang, H., Johnson, R., Martin, S., Kally, S., Kally, S., Khan, J., Lewis, L., Lit, Z., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulagedd, H., Lozado, R.J., Lu, X., Ma, J., Marbua, P., Martin, R., Martinez, E., Mangum, A., Mandra, E., Martin, R., Martinez, E., Mandra, S., McLedd, M. P., Moneil, T.Z., Meenen, E., Mandra, S., McLedd, M. P., Moneil, T.Z., Menen, E., Mandra, S., Morris, R., Martin, R., Martinez, E., Mandra, P., Martin, R., Martinez, E., Mandra, D., Newton, G., Olarnpunsagoon, A., Pal, S., Parks, K., Paul, H., Perez, A., Perez, L., Pfannkoch, C., C., Patternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Poindexter, A., Renter, M., Redier, M., Raijs, D., Sanders, W., Schertz, S., Sott, G., Shatsman, S., Shen, H., Sheel, M., Rose, M., Sodergren, E., Sotton, A., Tabor, P., Taylor, C. Steinle, M., Strong, R., Wang, C., Wang, Y., Walles, R., Warzen, B., Wang, C., Wang, R., Wang, C., Wang
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On Nov 15, 2002 this sequence version replaced gi:23265010.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs-scaffold, and there may be sequence contigs within a contigs-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dases 1 to 245104)
Rat Genome Sequencing Consortium.
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------ Summary Statistics
Assembly program: Phrasp; version 0.990329
Consenus quality: 202567 bases at least Q40
Consenus quality: 204753 bases at least Q20
Consensus quality: 205914 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Estimated insert size: 206745, sum-of-contigs estimation Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111077 TCAAACCAGAAAAAAGGCCTACAGCAGCATCTCCAGAGAGCATTAATCAATAGCCAAGAA
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Database :

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Total number of

Searched:

Title: Perfect score:

Sequence:

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Scoring table:

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                                                                                                                                                                                                 LysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAla
               HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet
                                                                           AspSerSerGlnProGluArgSerSerArgArgProArgGlnArgThrSerGluSer
                                                                                         601 TCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTG
                                                                                                                                                                                                                                                                                                                       SerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPhe
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                                                                                                                                                                                                                                                            SerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, TSC403; ING1L, diagnosis, lung cancer, cell cycle, regulation,
cell proliferation, cell aging, apoptosis, tumour suppressor, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human INGIL encoding cDNA with 5' and 3' untranslated regions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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/product= "ING1L"
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P-PSDB; AAY29606.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
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                                                                                                                                                                                                                                                                                                                          Human lung-specific gene TSC430 overexpressed in cancer tissue, used for treatment of, e.g. colon tumour
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Matches:
Conservative:
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page 91; 99pp; Japanese.
                                                                                                                                                                                                                                                 Ozaki K,
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98JP-0038133.
98JP-0073234.
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                                                                                                                                                                                                                                                                              WPI; 1999-494294/41, P-PSDB; AAY29606.
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Best Local Similarity:
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Pred. No.:
                                                                                                                         )2-FEB-1999;
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03-FEB-1998;
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                                                                                                                                                                                                                                                                                                                     Tumour suppressor; p471NG3; cell proliferation; cellular aging; p331NG2;
anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Tumour suppressor homologue protein, p33ING2"
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                                                                                   AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg
                                       812 TCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGA
                                                                                                                  872 GATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAGGATAGAAGATCGAGG
                    SerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tumor suppressor protein p471NG3 for the diagnosis and treatment
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                                                                                                                                                                                                                                                                                      suppressor homologue protein,
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P-PSDB; AAE06675.
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                             The present sequence represents the human tumour suppressor gene INGIL. The present invention also describes the human gene TSC403 expressed specifically in normal lung tissue. TSC403 is useful in the diagnosis, investigation and treatment of cancers in which it is overexpressed, including cancer of the lung, breast, fallopian tube, oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas. INGIL is useful in the investigation of cell proliferation, aging and apoptosis and the pathology of cancer, the diagnosis and treatment of cancer such as cancer of the colon, stomach, oesophagus or fallopian tube, and the screening of candidate drugs for the treatment of such
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                                                                                                                                                                                                                                  BP; 356 A; 206 C; 280 G; 236 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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Claim 15; Page 91-93; 99pp; Japanese.
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This sequence encodes the human tumour suppressor (TUSUP) protein. The TUSUP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential cAMP and cGMP dependent protein kinase phosphorylation site, nine potential protein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation site. TUSUP has structural and chemical similarity to p33. TUSUP can be used to tracts or of the immune system. Agonists of the TUSUP protein can be used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human tumour suppressor protein for treating cancer, particularly of reproductive and gastrointestinal tracts or immune system -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 AC-CGGCTGCTCACCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCAC
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P-PSDB; AAY52199.
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1153
                                                                           20-MAY-1999;
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                                LysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsnGlnLysLys
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                                                                                             GACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAAAATATCAAGAAACGTTA
                                                                                                                                                                                                       ArgleuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys
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                                                                                                                                                                                                                                                                                                                              HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLysAlaLysMet
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                SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
                                                                            AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumour suppressor protein; TUSUP; human; cancer; treat; prevent; reproductive tract; gastrointestinal tract; immune system; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= TUSUP
/note= "Tumour suppressor protein"
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247 GCGGTGATGTTTCCAACCTCTTTCCCAGTCAATGGATCAGGACGGCGATCAGCAGCTCGG 306
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                                                                                                                                                                                                                                                                                                                                              MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuThrGlyGluArg
                                                                                                                                                                                                                                                                                                                                                                                                           SerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367 TAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCTCCAGAGAGCACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rLysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIl
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                                                          The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodelling and osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone remodelling genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln-
                                                                                                                                                                 Sequence 1154 BP, 367 A; 216 C; 285 G; 265 T; 21 other;
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270
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Conservative:
Mismatches:
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                                Column 239-242; 206pp; English
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AAGAAAGAAGATGATTTAAACCAGAAGAACGTCTACAGCAGCTTCTCCAGAGAGCACTA
                                                                                                       ArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGly1le
                                                                                                                                                                                                                             AGACCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAATGGGATT
                                                                                                                                                                                                                                                                  GluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLysLysLys
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                                                                                                                                                                                                                                                                                                                                                 CGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAAT
                                                                                                                                                                                                                                                                                                                                                                                       GluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerThr
                          IleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeu
                                                         ATTAATAGTCAAGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG
                                                                                     ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu
                                                                                                                                                SerGluArgAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful an array for the diagnosis of bone remodeling and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
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208 AspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGly 227
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874.50
77.41%
61.11%
59.05%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with C ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the C p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 mor significant variations in its expression suggesting that ING1 was not a useful gene to study in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
ACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAA
                         nGlubroThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAs
                                        TGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTTTCACTTACCTATAAACCAAA
                                                                                                                             SGIyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSerTh
                                                                                                                                                       GGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTAC
                                                                          nGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProly
                                                                                                                                                                                                                                                                                                                                                                p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grigorian IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= P37ING1 polypeptide
                                                                                                                                                                                rGluLysThrLysLysAspArgArgSerArg 280
                                                                                                                                                                                                          TGAAAAGACAAAAAGGATAGAAGATCGAGG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
847..1686
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                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                                                        Murine P37ING1 coding sequence.
                                                                                                                                                                                                                                                             AAA53790 standard; cDNA; 2817
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                   Gene, each having their own promoter have been discovered.

Expression of one promoter (la) produces a protein identical to indentical to midentical to one promoter (la) produces a protein identical to indentical c-terminal fragment to ING1 but an additional 104

On identical C-terminal fragment to ING1 but an additional 104

Consider the constant of the newly discovered protein has been designated p371NG1 (Wild type ip33)NG31. p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an or isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the concogenic form of ing1. Novel peptide sequences taken from the 104 concogenic form of ing1. Novel peptide sequences taken from the 104 concogenic form of ing1. Novel peptide sequences taken from the 104 concogenic form of ing1. Novel peptide sequences taken from the 104 concogenic form of indetection methods for treatment of cell the prolypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1102 GATGAGAAGATCCCAGATCGTGAGTCAGATGGTGGAGCTGGAGGAGAACCGCAGCAGCAGAAGA
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alternative initiation exons of the ing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosing
ted nucleic
                                                                       LysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAsp
                                                                                                                                          Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                    CysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene, each having their own promoter have been discovered. Expression of one promoter (la) produces a protein identical to ING1. Expression of a second promoter (lb) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 h.terminal amino acids. The newly discovered protein has been designated p371NG1 (Wild type: p331NG1). p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                        p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
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                                                                                                                                                                                                                                                                                                                                                                                                      coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       those expressing wild type p53) p371NG1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p371NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
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Matches:
Conservative:
Mismatches:
Indels:
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75.74%
59.19%
57.63%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene; ss; monoclonal antibody; epitope; inhibitor of growth 1; ING1; tumour suppressor; cell cycle; breast tumour; lymphoid malignancy; cell growth; anti-ING1; CAb; isoform; diagnosis; tumour; antigen; p331NG1b.
                                                                                                         1006 AAGAAGAAGCGCTCCAAGGCCAAAGCGGAGCGAGAGGGGGGCGTCCCCTGCCGATC
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                                                                                GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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                                US-09-513-365A-1 (1-280) x AAH28478 (1-1533)
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The sequence is a variant of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine; ss
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(SLOK ) SLOAN KETTERING INST CANCER RES.
(CORR ) CORNELL RES FOUND INC.
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24-OCT-2000; 2000US-0602362.
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GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention discloses monoclonal antibodies which can be used, in combination, to specifically recognise epitopes of ING1 (inhibitor of growth 1) protein isoforms. ING1 is a tumour suppressor gene and its expression is regulated through the cell cycle, peaking in the S phase. Expression of ING1 is down regulated in breast tumours and lymphoid malignancies. Overexpression of a construct containing the ING1 gene is able to inhibit cell growth by reducing the fraction of cells which enter into the S phase. The monoclonal antibodies are useful for detecting an ING1 protein in a cell, which involves selecting a cell that ectopically or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAbl-CAbl0 (not defined), preferably a mixture of CAbl-CAb4, which can detect at least two or different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal (preferably, human) associated with aberrant levels of an ING1 protein. The antibody or animal contains the land of the human inhibitor of growth 1 (ING1) isoform, animal 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel monoclonal antibody which specifically recognizes epitope of ING1, inhibitor of growth 1 protein, and designated CAb1-10, useful for detecting two different isoforms of ING1 and diagnosing a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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                                                                                                 /product= "p33ING1b"
                                                Location/Qualifiers
873..1712
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26-FEB-1999; 99US-0258372.
15-NOV-1996; 96US-0751230.
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22-MAR-2000; 2000US-0532868
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(BOLA/) |
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1248 AGCGGCAAGGCTGGCGCGGACAGGCCCAAGGCGAGCGCGCAGCCTGACAAGCCC 1307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1668 AAAGCCCTGGAGAAATCCAAAAAAGAGAGG 1697
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us-09-513-365a-1.p2n.rng

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human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of the p53 gene many cases the mechanism of functional inactivation of tumours. In many cases the mechanism of functional inactivation of the p53 gene many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 nor significant variations in its revealed mutations in ING1 nor significant variations in its cancer etiology. However, alternative intitation exons of the ingl expression of one promoter (1a) produces a protein laving their own promoter have been discovered.

Expression of one promoter (1a) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 N-terminal amino acids. The newly discovered protein has been designated p37TNG1 (wild type: p331NG1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37ING1 has the cancer proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or transmal peptide of p37TNG1 can also be used in detection methods for the p37TNG1 variant.

The polypeptides may be useful in gene therapy for treatment of collegancy and proving a proving a page of the polypeptide may be useful in gene therapy for treatment of collegancy and page of the polypeptide page and page of the polypeptide of p
                                                                                                                                                          Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                      Grigorian IA;
                                                      Gurova KV,
                                                                                                                                                                                                                                                                          Claim 17; Fig 6; 134pp; English.
(UNII ) UNIV ILLINOIS FOUND.
                                                   Zeremski M,
                                                                                                         WPI; 2000-491278/43
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Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;

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CGCCGGGTACTGCACTGCATCCAGAGGCCCTGATCCGCAGCCAGGAGCTAGGCGATGAG 125
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Mismatches:
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Alignment Scores:
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                        246 AAGGCGGGCCAGGACAAGTCGAAGAGTGAGGCCATCACACAGGCAGATAAGCCGAATAAC 305
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                                                   150 ArgArgProArgArgArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGly
                                                                                                                     210 AsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of a human cancer associated antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knuth A,
LysAlaLysMetAspSerSerGlnProGluArg-
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(CORR ) CORNELL RES FOUND INC.
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24-OCT-2000; 2000US-0602362.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   604 AAGACCTCCAAGAAGAAGCGCTCCAAGGCGAAGGCGGAGGGGAGAGGCGTCCCCTGCC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCCAAGTGCCGGGGGGAGAACGAG 843
                                                        The present sequence encodes a human cancer associated antigen.

The sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polyynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                                                                                                                                                                                                                                               95
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 cloning) technique, useful in nucleic acid based therapies to treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                          116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-
                                                                                                                                               Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;
                                                                                                                                                                                   1143
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                    Page 44; 62pp; English.
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Best Local Similarity:
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LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A partial cDNA clone (AAT69651), designated ING1, codes for a novel tumour suppressor protein p331NG1 (AAM19118) that is a potent inhibitor of cell growth. It was isolated by subtractive the protein p31NG1 (BAM19118) that is a potent conversation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and Hela cDNA libraries. A complete ING1 sequence (AAT69652) was obtd. by 5'RACE. ING1 is localised to the 13q33-34 chromosome region, to which a number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer, a decreased level of ING1 mRNA indicates cancerous cells.
                                                                                                                               Tumour suppressor gene; ING1; p331NG1; breast cancer; brain cancer; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1902 BP; 574 A; 391 C; 461 G; 476 T; 0 other;
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08-DEC-1995;
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AAT69651;
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P-PSDB; AAW79674
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         LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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                                                                                                                            GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                                                        331 AAGCCC-----AACAGCAAGCGCTCACGGCGGCAGCGCAACGAGAACCGTGAGAAC 384
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brain tumour; gene therapy; tumour suppressor; ss.
                                                                                                                                                                                                                                                                                                                                                                            LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                               ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-
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                                                                                      WPI; 1998-542700/46
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Length:
Matches:
Conservative:
Mismatches:
Indels:

3.85e-60

728.00 74.79% 58.12% 49.16%

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Growth) partial cDNA clone that codes form a pl331NG1 polypeptide (see AAW79674), a novel inhibitor of cell growth and a candidate (see AAW79674), a novel inhibitor of cell growth and a candidate (see AAW79674), a novel inhibitor of cell growth and a candidate cumour suppressor. Into is a new gene that is expressed in normal mammary epithelial cells, but which is expressed in normal cot expressed in many primary brain tumours. To isolate ING1, a subtractive hybridisation of breast cancer cell line cDNAs was performed with CDNA from normal mammary epithelial cells, and subtracted cDNAs were cloned into retrovirus vector pLNCX. Following passage through a packaging line, normal mouse mammary epithelial cells were infected, and infected cells were infected into note mice. Putative transforming fragments from tumours were contoured mice. Putative transforming fragments from tumours were isolated by PCR (see AAV62299-1) and subcloned into LNCX. An ING1 fragment was obtained and used to screen normal human fibroblast and Heia call cDNA libraries. 2 clones were sequence (see AAV6229) was obtained by RACE. A claimed method to potentiate apoptosis in a eukaryotic cell involves administering an active p33ING1 peptide or an oligonucleotide encoding such as a peptide con an oligonucleotide encoding such as a peptide con an oligonucleotide encoding such as a peptide con an entaryotic cell involves administering an antisense oligonucleotide. Also claimed are a method for inhibiting apoptosis in a eukaryotic cell, an assay for determining the level of p33ING1 ectivity in a eukaryotic cell, and an isolated eukaryotic cell, and an entariants that may be used to induce disclassing eucharyotic cell, and an entariants that may be used to induce
Modulating eukaryotic apoptosis by increasing p331NG1 activity -using p331NG1 derivatives, to induce apoptosis in cancer cells, and in the investigation of apoptotic pathways
                                                                                                                                                                                                                                                                                                                                                                                                         the nucleotide sequence of a human ING1 (INhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis in eukaryotic cancer cells.
                                                                                                                                                                                                                                                                             Example 2; Fig 2; 66pp; English.
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porplantage or treating inflammation, or disorders associated with cell proliferation and apoptosis e.g. bone cancer, brain cancer, cervix cancer, adenocarcinoma, leukaemia, lymphoma or melanoma. They are particularly useful as models for developing human therapeutic targets, identifying therapeutic proteins, or serving as targets for the development of human therapeutic agents that modulate tumour suppressor protein activity in cells and tissues that express the tumour suppressor protein. Polypeptides of the invention are used for identifying agents that modulate their activity. They are useful for raising antibodies or eliciting an immune response; as a reagent in assays designed to quantitatively determine levels of the protein (or its binding partner or ligand) in biological fluids; or a markers for tissues in which the corresponding protein is preferentially expressed. The invention is also used as vaccines. The present suppressor generals located on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGluLys1leGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArgAlaSerAsp 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyr 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 GluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452 GACGAGAAGATCCAGATCGTGAGCCAGATGGTGGTGGTGGTGGTGGAGAACCGCACGCGCAG
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   polynucleotides. Sequences of the invention are useful for diagnosing
                                                                                                                                                                                                                                                                                                            528 G; 417 T; 0 other;
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Mismatches:
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CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; tumour suppressor protein; cell proliferative disorder; vaccine; inflammation; brain cancer; adenocarcinoma; cervix cancer; bone cancer; apoptosis; leukaemia; lymphoma; melanoma; therapy; chromosome 13; gene;
                                                                   LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal
                                                                                      GluPheAlaileAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                                                                                                     GluMetIleGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                           SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu
                                                                                                                                                                                                                                                                                            GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCAAGTGCCGGGGGGAGAACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human tumor suppressor proteins, useful for developing human therapeutic agents, or preventing or treating inflammation, or disorders associated with cell proliferation, e.g. bone cancer, brain
                               GACCTCCCCATCGACCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human tumour suppressor polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
161..1036
//trog= b
//troduct="Human tumour suppressor protein"
1037..1905
/*tag= c
                                                                                                                                                                                                                                                                                                                                          LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                            Human tumour suppressor protein encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-FEB-2001; 2001US-0793706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2002; 2002WO-US03235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A full-length cDNA clone (AAT69652), designated ING1, codes for a novel 33 kDa tumour suppressor protein p33ING1 (AAW19119), formerly c p33IG1, that is a potent inhibitor of cell growth. A partial clone (AAT69651) was isolated by subtractive hybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased cell proliferation, and use of the insert to screen normal human fibroblast and HeLa cDNA libraries. The complete ING1 sequence was then obtd. by 5'RACE. ING1 is localised to the 13q33-34 chromosome region, to which a c number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer; a decreased level of ING1 mRNA indicates cancerous cells. They can also be used in gene therapy methods to block the proliferation of cancer cells.
                                                                                                                                                       Tumour suppressor gene; ING1; p331NG1; breast cancer; brain cancer; diagnosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated tumour suppressor gene, ING1 - useful to develop products for inhibiting or increasing cell proliferation, in particular for treatment or diagnosis of cancer
                                                                                                                                    Tumour suppressor gene ING1 full-length cDNA
           268 LysSerThrGluLysThrLysLysAspArg 277
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/note= "reverse primer 4"
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note= "reverse primer 3"
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/note= "direct primer 2"
857..876
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/note= "direct primer
complement (763..782)
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16..900
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                                                                AAT69652 standard; cDNA; 2061
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95US-0569721.
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P-PSDB; AAW18119.
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08-DEC-1995;
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                                            RESULT 15
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LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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                                                                                                                                                                                                                                                                                                                                                   116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu-------
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136
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             Length:
Matches:
Conservative:
Mismatches:
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58.12%
49.16%
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Best Local Similarity:
Alignment Scores:
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                                                                            Query Match:
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Search completed: January 12, 2004, 19:43:20 Job time : 276 secs

Sequence 2061 BP; 602 A; 439 C; 515 G; 505 T; 0 other;

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AK048800

Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230071A14 product:inhibitor of growth family, member 1-like, full insert sequence.

AK048800.1 GI:26339579

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (house couse)

Mus musculus (house mouse)

Mus musculus (house mouse)
                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BIS46850
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                  - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                 22781392 seqs, 12152238056 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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BU332089 603869689 BG211544 RST31111

BU225297

AK048800 Mus AK083144 Mus Description

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RC3-FN014

BE839427

BU264721 603814832 BU226578 603796130 AL673816 AL673816

AI186701 qe82d12.x BE831862 RC6-MT006 AL874284 AL874284

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QTOQALETVURNRAQWELHSQCKODPAESRERADSKSKWDSSQPERSERSRERRGREG
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                      Yokohama,
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               RIKEN Yokohma Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
Exploration Research Group, RIKEN Genomic Sciences Center (GSC)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
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Matches:
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

LE (bases 1 to 2643)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayasuu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Karoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Karoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Karoh, H., Kawai, J., Kojima, Y., Salto, R., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazwi, Y., Salto, R., Saltoh, H., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatu, M. and Hayashizaki, Y. Yasunishi, A., Muramatu, M. and Hayashizaki, Y. Dya, T., Yasunishi, A., Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome
                                                                                                             Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                                                     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonada,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Nature 409 (6821), 685-690 (2001)
                                   High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) MAN 99279253
                        Carninci, P. and Hayashizaki, Y.
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Analysis of the mouse transcriptome based on functional annotation of 60,707 full-length cDNAs

L Nature 420, 563-573 (2002)

B (bases I to 2812)

Adachi, J., Alzawa, K., Akimura, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatau, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Katoh, H., Kawal, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Katoh, H., Kawal, J., Kojima, Y., Minazaki, A., Murata, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Murantsu, M. and Hayashizaki, Y.

Direct Suhmission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
RIKEN integrated sequence analygis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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/db_xref="taxon:10090"
/clone="C630016P10"
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/strain="C57BL/6J"
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AKO83144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1136 GTGTCCTACGGGGAGATGATAGGCTGTGACAATGAACAGTGTCCCATTGAATGGTTTCAC 1195
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                                                                                                                                                                                                                                                955
                                                                                                                                                                                                                                                                                                                                                                                                                              GluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGlu 199
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                   ATGGATTCCAGTCAACCGGAAAGATCTTCTAGAAGACCTCGAAGACAGAGGCACCAGTGAG
                                                                                                                                                                                                                                                                                                                                         Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                        LeuHisSerGInCysPheGlnAspProAlaGluSerGluArgAlaSerAsplysAlaLys
                                                                                           MetAspSerSerGlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGlu
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arawaha, M., Nishi, K., Kayosawa, H., Kondo, S., Yamanaka, I., Saito, T., Odjobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuo, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810011M06 product.inhibitor of growth family, member 1-like, full insert sequence.
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Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                          1199 TTTTCATGTGTTTCACTCACCCTATAAACCCCAAGGGGAAATGGTATTGCCCAAAGTGTAGG
                                                                                                                                                                                                   260 GlyaspasnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSer
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                           ValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHis
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria;
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//protein id="BAC3878"."
/db_xref="d1.2550287"."
/translation="MLGQQQQQQLYSSAALLTGERSRLLSCYVQDYLECVESLPHDMQ
RNVSVLRELDNKYQFTLKEIDDYYEKYKEDDSNGKKRLQOHLQRALINSQELGDEKJ
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SRDLCHMTNGIDDDCDQPPKERKSKSAKKKKRSKAKQBREASPVEFAIDPNEFYYCLC.
NQVSYGEMIGCDNEQQPIEWFHFSCVSLJYKPKGKWYCPKCRGDNEKTWDKSTEKTKK
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
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Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Tyvo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K.H., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. and Hayashizaki, Y. TITLE Functional annotation of a full-length mouse cDNA collection NEDLINE Nature 409 (6821), 685-690 (2001) REFERENCE 5 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs JOURNAL Nature 420, 563-573 (2002) REFERENCE 6 (bases I to 1464) AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Ano, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Pukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Kaukawa, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kaukawa, T., Hori, F., Imotani, K., Ishi, Y., Kondo, H., Kauka, M., Kauka, M., Kauka, M., Kauki, Y., Kondo, H., Kauka, M., Kauki, M., Y., Kondo, H., Kauki, M., Y., Kondo, H., Kaukiawa, T., Kato, H., Kawai, J., Koilana, Y., Kondo, H., Kaukia, M., Kaukia, M., Y., Kondo, H., Kaukia, M., Kaukia, M., Y., Kondo, H., Kaukia, Y., Kondo, H., Kaukia, M.,	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, Y., Okido, T., Owa, C., Shibata, Y., Shibata, Y., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshid, T., Yasunishi, A., Yoshida, K., Yoshido, M., Muramatsu, M. and Hayashizaki, Y.  TITLE Direct Submission JOURNAL Submited (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9226		PEATURES Location/Qualifiers 1. 1464 forganism="Mus musculus" forganism="Mus musculus" forganism="CS7BL/6J" fdb_xref="FANTOM DB:2810011M06" fdb_xref="reanis009" fdb_xref="reanis009" fclone="2810011M06" fissue type="whole body" fclone="1b="RIKEN full-length enriched mouse cDNA library" forlone="1b="RIKEN full-length enriched mouse cDNA library" dev stage="10, 11 days embryo" fore="1nhibitor of growth family, member 1-like fmote="inhibitor of growth family, member 1-like" fmote-"inhibitor of growth family, member 1-like"	

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Eukaryota; Maves; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 736)
Boardan, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A.; Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
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                           142 GACATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAAAATATCAAGAACGTTA
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             AspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeu
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                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 912)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLCM2058 row: h column: 10 High quality sequence stop: 587.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
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JOURNAL
COMMENT
RESULT 4
BQ277444
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662

542

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/constructed from initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
/collowing this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI , size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (Bases I to 892)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bogch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                         BU332089 892 bp mRNA linear EST 28-NOV-2002
603869689F1 CSEQCHN65 Gallus gallus cDNA clone ChEST894a23 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                              HisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCys 258
                                                                                                                                                                                                                                                           GlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysProlleGluTrpPhe
                     GAGGTTTCACCCGTGGAGTTTGCGATTGATCCCAATGAACCGACTTACTGCTTATGTAAC
                                                                                                                                                 179 LysGluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArg
                                                                  GluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsn
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    .892
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Tel: 01612008930
Fax: 01612360409
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Matches:
Conservative:
Mismatches:
Indels:
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Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute o
                                                           PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                        /organism="Gallus gallus"
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                                                                                                                               Location/Qualifiers
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85.95%
75.83%
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Nature Biotechnology, in press. Note that even though the
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expressed in HT1080 under normal circumstances."
                                                                                                                      Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McBligott, K., Boozer, S., Mays, R., Smith, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 919)
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214
7
7
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Tel: 216 431 9900
Fax: 216 361 9596
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 Email: scain@athersys.com
                GI:13733231
                                                                                                                                                                                                                                                                    11329013
Contact: Scott J. Cain
Athersys, Inc.
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1096.50
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                                             Homo sapiens (human)
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rounds using conditions adapted from Soares et a (1994) 91: 9228-9232 and Bonaldo et al., Genome (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                           892
210
18
16
                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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BIS48536 778 bp mRNA linear EST 05-SEP-2001 603191255F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5262540 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mismatches:
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Gaps:
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// Mol_type="mRNA" |
/ Ab Zref="taxon:9606" |
/ Alone="INAGE:394165s" |
/ Lissue_type="small cell carcinoma" |
/ Lispue="small carcinoma" |
/ Lispue="small cell carcinoma" |
/ Lispue="small carcinoma" |
/ Lispue="sm
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BE796780
BE796780.1 GI:10218080
EST.
                                   217
                                                                                                                                   AGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATGC 483
                                                                                                                                                                                    PheHisPheSerCysValSerLeuThrTyrLysProLysGlyLysTrpTyrCysProLys 257
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304 AGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATGATCAGCCA 363
                                                                                                                                                                                                                                                                                        CysArgGlyAspAsnGluLysThrMetAspLysSerThrGluLysThrLysLys----
                                                                                                           198 ArgGluAlaSerProValGluPheAlaIleAspProAsnGluProThrTyrCysLeuCys
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/organism="Homo sapiens"
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  University of Manchester Institute of Science and Technology (UMIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 uAspAsnLysTyrGluCluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLy
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193
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Matches:
Conservative:
Mismatches:
                                                                                                                                                           /organism="Gallus gallus"
/mol type="mRNA"
/strain="White Leghorn, Hisex"
/db xref="texon:9031"
/clone="ChEST531f23"
                       )
PO Box 88, Manchester, M60 1QD, UT
Tel: 01612008930
Fax: 01612360409
Email: Simon Hubbard@unist.ac.uk:
Location/Qualifiers
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Bong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysValSerLeuThrTyrLysBrolysGlyLysTrpTyrCysProLysCysArgGlyAsp 261
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                      GAAATAGACGACGTCTATGAAAAATACAAGTCTGAGAACGATCCTGCTCAGAAGAAACGC
                                                                                                                                                                                                                                                       TIGCAGCAGCACCTCCAGCGGGCTTTAATCAACAGTCAAGAACTCGGAGAGATGAAAATT
                                                                                                                                                                                                                                                                                                          Gln11eValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGlnMetGluLeuHis
                                                                                                                                                                                                                                                                                                                                        SerGinCysPheGinAspProAlaGluSerGluArgAlaSerAspLysAlaLysMetAsp
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603581891F1 CSEQCHN75 Gallus gallus CDNA clone ChEST531f23
    0013
  Conservative:
Mismatches:
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Department of Biomolecular Sciences
                                                                                                    US-09-513-365A-1 (1-280) x BU259874 (1-779)
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BU386788
BU386788.1 GI:25894789
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Gallus gallus
94.06%
88.13%
70.43%
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  Percent Similarity:
Best Local Similarity:
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                     Best Local
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I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.

TAG LIBBUL-CF-ENI
TAG TISSUE-Human bung Epithelial Cell Lines untreated LPS 6hr to LBS 24h
TAG SEQ-CTGCTCAGGT"

a 161 c 114 g 280 t
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603489003F1 CSEQCHN63 Gallus gallus cDNA clone ChEST388e2 5', mRNA
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mismatches:
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clonellib="ULCF-ENI"

/note="Organ: Lung; Vector: pT773-pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UL-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
CDNA was ligated to an EcoR I adaptor, digested with Not
                                                                                                                                                                                                                                                                                                                                                                                                                 BM982877 175 bp mRNA linear EST 21-FEB-2003 UI-CF-EN1-acs-d-05-0-UI.SI UI-CF-ENI Homo sapiens cDNA clone UI-CF-ENI-acs-d-05-0-UI 3', mRNA sequence.
                                                                                     541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCray Lab
University of Iowa
University of Iowa
University of Iowa
Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Clone Of the Company of Iowa
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: On or from Open Biosystems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 735)
Bonaldo, M. F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                            CTGCGACGATCAGCCACCTAAAGAGAAAAGATCGAAATCTTCCAAGAAGAAAAAACGCTC
                                          rLysklaLysGlnGluArgGluAlaSerProValGluPheAlaIleAspProAsnGluPr
                                                                                                                           OThrTyrCysLeuCysAsnGlnValSerTyrGlyGluMetIleGlyCysAspAsnGluGl
                                                                                                                                                    GACTTACTGCTTATGTAACCAAGTGTCTTACGGCGAAATGATGATGATGTGATAACGAACA
                                                                                  CAAAGCCAAACAAGAGGGAGGTTTCACCCGTGGAGTTTGCGATTGATCCCAATGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-ENL-acs-d-05-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
/cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .735
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (www.openbiosystems.com)
Seg primer: M13 FORWARD
POLYA=Yes.
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Homo sapiens
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MNH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                rSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspGlnPr
                                                                                                                                                                                                                                                                                                                                                                                                                                495 ACCTAAAGAGAAAAGATCGAAATCTTCCAAGAAAAAAAACGCTCCAAAGCAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov.a column: 07
                                                                                             315 GATGGAAACACTCTCAGTGTTTTCAGGATCTGTCTGAAAACGACAAGCCTCTGGAAAA
                                                                                                                                                   OProLysGluLysLysSerLysSerAlaLysLysLysLysArgSerLysAlaLysGlnGl
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                                     nMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAspLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Bmail: cgapbs-r@mail.nih.gov
Tissue Prcourrement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
CDNA Library Preparation: Catherine Lee, Endocrine Pancreas
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/clone|lip="CSEOCHNG3"
/clone|lip="CSEOCHNG3"
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/compatible sites of a custom and subsed."
/clone|lib="CSEOCH"
/compatible sites of a custom andified from Soares et al., PNAS (1994): 791, except that a significantly longer
/compatible sites of a custom andified from Soares et al., Genome Research 6 (1996): 791, except that a significantly longer
                                                                                                                                                                                                                                                                      Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 707)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, B.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
Cuprehensive Collection of Chicken cDNAs
Cuprehensive (22), 1965-1969 (2002)
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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| /db xxef="texcn:9606" |
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| /n
Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J. L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith
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  Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McBlligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Alika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J., and bucar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, C
Tel: 216 431 9900
Fax: 216 361 9596
Email: Scain@athersys.com
High quality sequence stop: 531
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 798)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
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RST2972 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
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222 TyrGlyGluMet1leGlyCysAspAsnGluGlnCysProlleGluTrpPheHisPheSer 241	242 CysValSerLeuThrTyrLysBroLysGlyLysTrpTyrCysBroLysCysArgGlyAsp 261	262 AsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg 280 	Search completed: January 12, 2004, 20:28:52 Job time : 2038 secs
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; Sequence 6 Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; TITLE OF INVENTION: Human TSC403 gene and human INGIL gene
; FILE REFERENCE: 060193
; CURRENT APPLICATION NUMBER: US/09/601,478
; CURRENT FILING DATE: 2000-08-03
; PRIOR FILING DATE: 1998-04-28
; PRIOR FILING DATE: 1998-04-28
; PRIOR FILING DATE: 1998-03-05
; PRIOR FILING DATE: 1998-03-05
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; COFTWARE PATENTION NUMBER: 20 H10-38133
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11
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US-09-499-082-9
US-09-258-372-9
US-09-158-372-9
US-09-106-783A-2
US-09-105-286-2
US-09-195-286-2
US-09-195-286-2
US-09-105-286-2
US-09-105-286-3
US-09-620-312D-435
US-09-620-312D-435
US-08-990-571-77
US-08-990-571-37
US-08-990-571-37
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ORGANISM: Homo sapiens
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1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                  nucleic search, using frame_plus_p2n model
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US-09-601-478-7
US-09-484-970B-81
US-09-006-783A-4
US-09-258-257-1
US-09-258-371-1
US-08-569-711-1
US-08-571-230-1
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Result No.

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Matches:
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                                                                        OTHER INFORMATION: human
PatentIn Ver.
                                                  sapiens
                                                                                   ; NAME/KEY: CDS
; LOCATION: (92)..(931)
US-09-601-478-7
                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                    TYPE: DNA
ORGANISM: Homo
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Pred. No.:
                        LENGTH: 1078
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| Sequence 7, Application US/09601478
| Sequence 7, Application US/09601478
| Patent No. 6403788-5
| GENERAL INFORMATION:
| APPLICANT: Ostuka Pharmaceutical Co., Ltd.
| TILE OF INVENTION: Human TSC403 gene and human INGIL gene
| FILE REFERENCE: Q60193
| CURRENT APPLICATION NUMBER: US/09/601,478
| CURRENT FILING DATE: 2000-08-03
| PRIOR PAPLICATION NUMBER: JP H10-134679
| PRIOR FILING DATE: 1998-04-28
| PRIOR FILING DATE: 1998-03-05
| PRIOR PAPLICATION NUMBER: JP H10-33134
| PRIOR PAPLICATION NUMBER: JP H10-38133
| PRIOR FILING DATE: 1998-02-03
| NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                            607 AAGACCCCGCAGCCAGCGACCAGTGAAAGCCGTGATTTATGTCACATGGCAATGGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09006783A
Patent No. 6297366
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey V
APPLICANT: Garkavetev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 rGluLysThrLysLysAspArgArgSerArg 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   967 TGAAAAGACAAAAAGGATAGAAGATCGAGG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: NO. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEPAX: 312-913-0002
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LENGTH: 873 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Illinois
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US-09-006-783A-4
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261 AspAsnGluLysThrMetAspLysSerThrGluLysThrLysLysAspArgArgSerArg 280
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                               GATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAGATAGAAGATCGAGG
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6426186 197886.1CB1
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Mismatches:
Indels:
Gaps:
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                                                                                                                   | Sequence 81, Application US/09484970B | Patent No. 6426186 | GENERAL INPORMATION: GENERAL INPORMATION: APPLICANT: Jones, Karen A. APPLICANT: Volkmuth, Wayne APPLICANT: Walker, Michael G. TILLE OF INVENTION: BONE REMODELING GENES FILE REFERENCE: PB-0014 US CURRENT APPLICATION NUMBER: US/09/484,970B | CURRENT FILING DATE: 2000-01-18 | NUMBER OF SEQ ID NOS: 172 | SOFFWARE: PERL PROGram
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Matches:
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81.57%
90.07%
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LOCATION: 17-37
OTHER INFORMATION:
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Best Local Similarity:
                                                                                  RESULT 3
US-09-484-970B-81
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96 LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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136
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                                                            Sequence 1, Application US/09258257
Patent No. 5965398
GENERAL INFORMATION:
APPLICANT: GREKAVYSEV, IGOR
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                           ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria STATE: Virginia COUNTRY: United States
ZIP: 22313-1404
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-513-365A-1 (1-280) x US-09-258-257-1 (1-1902)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 854-7400
TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
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58.12%
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Best Local Similarity:
Query Match:
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US-09-258-257-1
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                     RESULT 5
US-09-258-257-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 -----AACÁGCAAGCGCTCACGGCGGCAGCGCAACCAACGAGAACCGTGAGAACGCGTCC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 GTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTGGGCAAC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GluThrieulysGluIleAspAspValTyrGluLysTyrLysLysGluAspAspLeuAsn 77
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382 AGCGGCAAGGTTGGCGGACGGACAGGCCATGCGGTAGCGCAGTCTGACAAGCCC
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                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                               US-09-513-365A-1 (1-280) x US-09-006-783A-4 (1-873)
                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                          6.3e-86
853.50
75.74%
59.19%
57.63%
STRANDEDNESS: single
                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                    7..813
                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                          ; NAME/KEY:
; LOCATION:
US-09-006-783A-4
                                                                                                                                                                                         Alignment Scores:
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Matches: Conservative: Mismatches: Indels:

Length:

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US-09-513-365A-1 (1-280) x US-09-258-371-1 (1-1902)
                                                                                                                                                              728.00
74.79%
58.12%
49.16%
   nucleic acid
EDNESS: double
                                                                          CDS
109..741
                               TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                  STRANDEDNESS:
                                                                         , NAME/KEY:
; LOCATION:
US-09-258-371-1
                                                                                                                                    Alignment Scores:
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                                                     271 GGCAACAGCGGCAAGGTTGGCGCGGCGGAAGGCCGATGGCGGTAGCGGCAGTCTGAC 330
                                                                                     144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
                                                                                                       164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                                                                                                               GCGTCCAGCAACCACGACCACGACGACGCCTCGGGCACACCAAGAAGAAGAAGAAGAAGAAGGCC 444
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CGGCAGGTGGACACCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
                            -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 08/751,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mooi, Leelie A.
REGISTRATION NUMBER: 37,047
REFRENCE/POCKET NUMBER: 0287;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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LeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAla 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 CGCCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGACACAGTG 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 AAGACCTCCCAAGAAGAAGAAGCGCTCCAAGGCCGAGCGGAGCGAGGCGAGGCGCGTCCCCTGCC 504
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                                                                                                                         76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu 95
56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                     204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
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Patent No. 6037121
GENERAL INFORMATION:
APPLICANT: GARKAVTSEV, Igor
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244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
164 CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer 183
                                                                              LysSerAlaLysLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
                                                                                                                                                                                                                                                                                                                                                    GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                                   385 GCGTCCAGCAACCACGACCACGACGACGCCCTCGGGCACACCCAAGGAGAAGAAGACCC
                                                                                                                                                              204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                    264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTITE: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGGNT INPORMATION:
NAME: MOOJ, Lealie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODIN
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESSONDENCES: 23
ADDRESSEE: Burns, Doane, Swecker & Mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08751230 Patent No. 6117633
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu------
                                                                                            STREET: P.O. Box 1404
CTTY: Alexandria
STREET: P.O. Box 1404
CTTY: Alexandria
STATE: Usinia
STATE: Usinia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,721A
FILING DATE: 08-DEC-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                DNA SEQUENCE ENCODING A TUMOR SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MOOI, Leslie A. REGISTATION NUMBER: 37,047
REPERENCE/DOCKET NUMBER: 028722-128
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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58.12$
49.16$
                   TITLE OF INVENTION: DN
TITLE OF INVENTION: SU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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; LOCATION:
US-08-569-721A-1
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                                                                                                       Version #1.30
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Conservative:
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Indels:
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                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATTORNEX/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
                                                                                   SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
                   ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
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STRANDEDNESS: double
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CLASSIFICATION:
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US-09-499-082-1
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APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Johnston, Randall N.
APPLICANT: Johnston, METHODS OF MODULATING APOPTOSIS
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENES: ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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Length:
Matches:
Conservative:
Mismatches:
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Patent No. 6143522
GENERAL INFORMATION:
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APPLICANT: Garkavtsev, Igor
APPLICANT: Raiabowol. Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
136
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                 Conservative:
Mismatches:
Indels:
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ZIP: 22313-1404
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                                                     LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal 203
                                                                                                                                                  625 GGGCTCAATCATAAACCCAAGGGCAAGTGGTACTGTCCCCAAGTGCCGGGGGGAGAACGAG 684
                                                                          385 GCGTCCAGCAACCACGACCACGACGACGCCCTCGGGCACACCCAAGGAGAAGAAGCC
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APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burne, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VA
COUTRY: USA
ZIP: 2213-1404
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MOOJ, L68116 A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287:
TELEPHONE: 415-854-7400
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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; LOCATION: 109.
US-09-258-372-1
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Pred. No.:
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us-09-513-365a-1.p2n.rni

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244 SerLeuThrTyrLysProLysGlyLysTrpTyrCysProLysCysArgGlyAspAsnGlu 263
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                            GluMetIleGlyCysAspAsnGluGlnCysProIleGluTrpPheHisPheSerCysVal
204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
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                                                                                                                                                                                                                                                                                             264 LysThrMetAspLysSerThrGluLysThrLysLysAspArg 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Garkattsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
STREET: 699 Prince Street
CITY: Alexandria
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION S14
PRIOR APPLICATION S14
PRIOR APPLICATION DATE: US-NOV-1995
ATFORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 37,047
REJERBRENCE/DOCKET NUMBER: 37,047
TELERBRANCE/DOCKET NUMBER: 37,047
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/08751230; Patent No. 6117633; GENERAL INFORMATION:
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49.16%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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; LOCATION: 16.
US-08-751-230-9
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Best Local Similari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SerGluArgAlaSerAspLysAlaLysMetAspSerSer 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu 163
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136
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14
          COMPUTER: REALCHELE FORM:

COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
CORFRANTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
PILING DATE:
APPLICATION NUMBER: 08/751,230
FILING DATE:
APPLICATION NUMBER: 08/751,230
FILING DATE:
APPLICATION NUMBER: 37.047
REGISTRATION NUMBER: 37.047
REFERENCE/POCKET NUMBER: 37.047
REFIRENCE/POCKET NUMBER: 37.047
REFIRENCE/POCKET NUMBER: 02872-144
TELEFORMICATION INFORMATION:
TELEFORM: 415-854-7400
TELEFAK: 415-864-7400
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2061 base pairs
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74.79%
58.12%
49.16%
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STRANDEDNESS: double
COMPUTER READABLE FORM:
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US-09-258-371-9
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Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-513-365A-1 (1-280) x US-09-499-082-9 (1-2061)
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                                                                                                    FILING DATE: 2'-MA-139'
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATORNEY/AGENT INFORMATION:
NAME: MOOI, LeSlie A. 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
APPLICATION NUMBER: US/09/499,082
                                                                             US/08/828,158
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728.00
74.79%
58.12%
49.16%
                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/06
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 06
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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16..900
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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DB:
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                    TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
APPLICANT: Riabowol, Karl
APPLICANT: Conneton, Randall N.
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSPEN: 699 Prince Street
CITY: Alexandria
STREET: 699 Prince Street
CITY: Alexandria
STRATE: VBA
COUNTRY: USA
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Patent No. 6143522
GENERAL INFORMATION:
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US-09-499-082-9
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                                                                                              116 ArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu------- 130
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                          184 LysSerAlaLysLysLysArgSerLysAlaLysGlnGluArgGluAlaSerProVal
                                                                          76 LeuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGlnGlu
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       56 TyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAspAsp
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TITLE OF INVENTION: METHOD OF MODULATING P53 ACTIVITY
FILE REPERENCE: 02872-181
CURRENT APPLICATION NUMBER: US/09/159,871A
CURRENT FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: US 60/060,138
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1998-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-159-871-1
Sequence 1, Application US/09159871A; Patent No. 6420136; GENERAL INFORMATION:
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LOCATION: (16)..(897)
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SEQ ID NO 1
LENGTH: 2061
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ZIP: 22313-1404

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Garkattsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: SUPPRESSOR GENE INGI
TUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
TELEPAX: 415-854-8275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
                                                                                                                                                                                                                                                                                             ; Sequence 9, Application US/09258372
; Patent No. 6238918
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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Query Match:
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664 GACCTCCCCATCGACCCCAACGAACCACTGTCTGTGCAACCAGGTCTCCTATGGG 723
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136
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      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                US-09-513-365A-1 (1-280) x US-09-159-871-1 (1-2061)
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Job time : 84 secs
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January 12, 2004, 17:22:12; Search time 430 Seconds (without alignments) 8721.912 Million cell updates/sec
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/ cgnz_6/ptodata/2/pubpna/US06 NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMEDIES

		d			SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	1046	96.9	1078	14	US-10-115-899-7	Sequence 7. Appli
7	838.4			14	US-10-115-899-6	Sequence 6, Appli
m	378.4		421	11	US-09-918-995-37033	Sequence 37033, A
4	237.4			11	US-09-968-653A-4	Sequence 4, Appli
	183.4			10	US-09-764-877-3454	Sequence 3454, Ap
9	182.2			11	US-09-968-653A-2	Sequence 2, Appli
7	174.4			11	US-09-968-653A-6	Sequence 6, Appli
80	91.6			13	US-10-117-722-435	Sequence 435. App
0	91.6			15	US-10-037-270-435	Sequence 435, App
10	83.6	7.7	451	10	US-09-738-973-146	Sequence 146, App
11	83.6			10	US-09-854-133-146	Sequence 146, App
12	83.6					Sequence 146, App
13	9.99		993	10		Sequence 257, App
14	62	5.7		10	US-09-938-842A-1178	Sequence 1178, Ap
	9	ď			713-09-908-975-12517	G 513C1 annothing

Sequence 23744, A	Sequence 16047, A		Sequence 5815, Ap		Sequence 18240, A	Sequence 4582, Ap		Sequence 2, Appli	Sequence 5212, Ap		262		126.	2503	1502,	Sequence 6502, Ap	750	Sequence 502, App	Seguence 5502, Ap	Sequence 43, Appl	14,	Sequence 863, App	5	Sequence 90, Appl	486	1,	491	Sequence 7, Appli	22
US-09-908-975-23744	US-09-918-995-16047	US-10-032-585-6348	US-09-814-353-5815	US-09-814-353-12097	US-09-814-353-18240	US-09-960-352-4582	US-09-919-580-114		US-09-814-353-5212	US-09-814-353-11499	US-09-871-161-262	US-10-311-455-298	US-09-960-352-12673	US-10-128-714-2502	US-10-128-714-1502	US-10-128-714-6502	US-10-128-714-7502	US-10-128-714-502	US-10-128-714-5502	US-10-001-887-43	US-10-240-452-14	US-10-106-698-863	US-10-240-453-100	US-10-239-676-90	US-10-311-455-486	US-10-312-841-1		US-10-311-455-7	US-10-311-455-227
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5.4	5.3	5.0	4.9	4.9	4.8	4.8	4.7	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3
58.6	56.8	54	52.8	52.8	51.6	51.6	50.8	49.6	49.2	49.2	49	49	48.8	48.6	48.6	48.6	48.6	48.6	48.6	48.4	48.4	48	47.6	47.6	47.6	47.6	47.2	47	46.8
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## ALIGNMENTS

US-10-115-899-7

i Sequence 7, Application US/10115899

i Publication No. US20020151025A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Human T5C403 gene and human ING1L gene
FILE REFERENCE: Q60193
CURRENT APPLICATION WUMBER: US/10/115,899
CURRENT FILING DATE: 2000-08-03
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-04-28
PRIOR FILING DATE: 1998-03-36
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION WUMBER: JP H10-134679
PRIOR APPLICATION WUMBER: JP H10-3343
PRIOR FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 1078
TYPE: DNA
CRGANISM: Homo sapiens
PELNGTH: 1078
TYPE: DNA
COTHER INFORMATION: human embryonic brain CDNA library
NAME/KEY: CDS
LOCATION: (92)...(931)
US-10-115-899-7

QUELY MATCH
GENERAL SIMILARITY 99.5%; Pred. No. 4.5e-240;
Best Local Similarity 99.5%; Pred. No. 4.5e-240;
Best Local Similarity 99.5%; Pred. No. 4.5e-240;
Matches 1049; Conservative 0; Mismatches 5; Indels 0; Gaps

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| GENERAL ANTOCALLANDER |
| CHARLAL ANTOCALLANDER |
| TITLE OF INVENTION: Human TSC403 gene and human INGIL gene |
| TITLE OF INVENTION: Human TSC403 gene and human INGIL gene |
| FILE REPERBENCE: O60193 |
| CURRENT APPLICATION NUMBER: US/10/115,899 |
| CURRENT FILING DATE: 2002-04-05 |
| PRIOR APPLICATION NUMBER: 09/601,478 |
| PRIOR FILING DATE: 1998-03-03 |
| PRIOR PILING DATE: 1998-04-28 |
| PRIOR PILING DATE: 1998-03-05 |
| PRIOR PILING DATE: 1998-03-05 |
| PRIOR PILING DATE: 1998-03-05 |
| PRIOR FILING DATE: 1998-02-03 |
| NUMBER OF SEQ ID NOS: 11 |
| SOFTWARE: PatentIn Ver. 2.1 |
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                                                                                                                                                                                                                                                                                                                                                                77.6%; Score 838.4; DB 14; 99.9%; Pred. No. 2e-190; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.9
Matches 839; Conservative
                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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US-10-115-899-6; Sequence 6, Application US/10115899; Publication No. US20020151025A1

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Publication No. US20030073084A1
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                                                                                                                                                                                                                                                                       APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROOM VARIOUS CDNA LIBRARIES
FILLE NEFERINCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILLING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37033
LENGTH: 421
                                                                                                                                                                                                                           Sequence 37033, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
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RESULT 4 US-09-968-653A-4 ; Sequence 4, Application US/09968653A

RESULT 4

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Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
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NAME: No. US20030073084Alnan, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/006,783A
PILING DATE: 15-JAN-1998
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 7..813
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TELEPHONE: 312-913-0001
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SEQUENCE CHARACTERISTICS:
LENGTH: 873 base pairs
TYPE: nucleic acid
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-913-0002
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59.0%;
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COMPUTER READABLE FORM:
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                                           -----CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGA
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                                                                                                                AAGATCTTCAAGAAGACCCCCCCAGCGGCACCAGTGAAAGCCGTGATTTATGTCACAT
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Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: UJ OCt-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6888 GGACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 6920
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NAME: No. US20030073084Alnan, Kevin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hu
STREET: 300 South Wacker Drive
CITY: Chicago
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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GGCGCAGCAGGAGCTGGGCGACACAGTGGGCAACAGCGGCAAGGTTGGCGCGGACAGGCC 407
                                                                                                                                                                                                                                                                                                                               595 GCCACCTAAAGAAAAGAAATCCAAGTCAGCAAAGAAAAAGAAACGCTCCAAGGCCAAGGA
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                                                                             477 AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNCE: PC005
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
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Pred. No. 5.5e-33;
0; Mismatches 266;
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Sequence 3454, Application US/09764877
Patent No. US20020147140A1
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CORGANISM: Homo sapiens
US-09-764-877-3454
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LENGTH: 8487
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522 CCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAG 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 174.4; DB 11;
Pred. No. 1.6e-31;
0; Mismatches 126;
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                                                                                                                                                    ADDRESSEE: McDonnell Boehnen Hulbert
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REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/968,653A FILING DATE: 01-Oct-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION UNMERS: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COCATION: 1..630

SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-968-653A-6
                                                                                                                                                                                                     STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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              Pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         882 AGACAAAAAGGATAG 897
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Best Local Similarity 66.5%;
Matches 250; Conservative
                                                      NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747 GAIGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT 806
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Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 2061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
16.9%; Score 182.2; DB 11; Length
Best Local Similarity 56.9%; Pred. No. 4.5e-33;
Matches 393; Conservative 0; Mismatches 268; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAAAGCCCTGGAGAATCCAAAAAAGAGAG 884
                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-968-653A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/0996853A Publication No. US20030073084A1 GENERAL INFORMATION:
LENGTH: 2061 base pairs
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                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                           MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -09-968-653A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 91.6; DB 15; Length 1864; 64.8%; Pred. No. 2.1e-11; ive 0; Mismatches 74; Indels 0;
                                              APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFRENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT APPLICATION NUMBER: US/52,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOSTWARE: pt_FL_Genes Version 1.0
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APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Elliot, Mark
APPLICANT: Bliot, Mark
APPLICANT: Mannion; Jane
APPLICANT: MINENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  734 GGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATGGTT
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CURRENT FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 146, Application US/09738973
Patent No. US20020110563A1
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Lodes, Michael J.
Fling, Steven P.
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Best Local Similarity 64.8
Matches 136; Conservative
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Wang, Zhiwei
Tillinghast,
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                             APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Ashudi, Vinod
APPLICANT: Ashudi, Vinod
APPLICANT: Ashudi, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744A1e1 Nucleic Acids and
TITLE OF INVENTION: No. US2003021974A1e1 Nucleic Acids and
TITLE OF INVENTION: No. US2003020404
FILE REFERENCE: 784CTP2BCIP
CURRENT APPLICATION NUMBER: 09/620,312
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
SOFTWARE: Pt_genes Version 1.0
SEQ ID NO 435
LENGTH: 1864
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Pred. No. 2.1e-11;
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5. US20030104529A1
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Best Local Similarity 64.8%;
Matches 136; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Kehrman, Tom
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Jian-Rui
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Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY; CDS
; LOCATION: (164)..(1420)
US-10-117-722-435
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Query Match
Best Local Similarity 58.6
Matches 163; Conservative
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Madden, Kevin
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Silva, Jeff
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Cali, Brian
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ORGANISM: Homo sapien
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                                                                                                                                   GGACAA 228
                                                                                                                                                                                                                                                          GAAATACCAAGAATCCTGAAGGAGCTAGACGAGTGCTACGAGGCGCTTCAGTCGCGAGAC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 AGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCG 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 AGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCG 408
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                                                                                                                                                                                             CATCGAGTCCCTGCCTTTCGACTTGCAGAAATGTCTCGCTGATGCGGGAGATCGACGC 75
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                                                                                                                                                                                                                                                                                                                                                                                          289 IGATITAAACCAGAAGAAACGICTACAGCAGCIICICCAGAGAGCACIAAITAAIAGICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Monamath, Readoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Darin R.
APPLICANT: Benson, Darin R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT APPLICATION NUMBER: US/09/854,133
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                   1;
      Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 451;
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                                                                0; Mismatches 114;
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0; Mismatches 114;
   DB 10;
   Score 83.6; DB 1/
Pred. No. 7.3e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 146, Application US/09854133 Publication No. US20020183499A1 GENERAL INFORMATION: APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.78;
1.7%;
ilarity 58.6%;
Conservative
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Best Local Similarity 58.6°
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapien
                              Similarity
Query Match
Best Local Simi
Matches 163;
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-09-854-133-146
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IITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GAAATACCAAGAGATCCTGAAGGAGCTAGACGAGTGCTACGAGCGCTTCAGTCGCGAGAC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 IGATITAAACCAGAAGAAACGICTACAGCAGCITCICCAGAGAGAGCACTAATTAATAGICA 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 AGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCG 408
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Sequence 146, Application US/10144649A
| Publication No. US20030118599A1
| GENERAL INFORMATION
| APPLICANT: Lodges, Michael J.
| APPLICANT: Mang, Tongtong
| APPLICANT: Fan, Liqun
| TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
| CURRENT APPLICATION NUMBER: US/10/144,649A
| CURRENT FILING DATE: 2002-08-21
| NUMBER OF SEQ ID NOS: 149
| SOFTWARE: FREESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 114;
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Pred. No. 7.3e-10;
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CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 09/487,558 PRIOR FILING DATE: 2000-01-19
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US-09-801-368-257
; Sequence 257, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. US20020128250Alman,
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APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Warge, Xun
APPLICANT: Warge, Xun
APPLICANT: Warge, Xun
APPLICANT: Warge, Xun
APPLICANT: Du, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SOU1-08-24
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1178
LENGTH: 813
                                                                                                                                                                                                                                                                                                                                                                              698 GAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAT 757
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                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                     Query Match 6.2%; Score 66.6; DB 10;
Best Local Similarity 66.2%; Pred. No. 1.4e-05;
Matches 96; Conservative 0; Mismatches 49;
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Pred. No. 0.00016;
0; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           818 GGGAAATGGTATTGCCCAAAGTGCA 842
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 257
LENGTH: 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-938-842A-1178
; Sequence 1178, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
                                                                                                                                                                                          ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.7%;
Best Local Similarity 65.1%;
Matches 108; Conservative
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RESULT 15 US-09-908-975-12517

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

January 12, 2004, 16:38:42 ; Search time 93 Seconds (without alignments) 5125.740 Million cell updates/sec Run on:

Title: Perfect score:

Sequence:

Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

569978 seqs, 220691566 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA: Database:

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/pcTu3\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/pcTu3\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			•			SUMMARIES		
Result No.	ult No.	Score	% Query Match	* Query Match Length	DB	a	Description	
;	-	7707			•		-	
	4	0 # O T	70.7	7018	ť	US-09-601-4/8-/	sednence /, Appli	
	7	838.4	77.6	840	4	US-09-601-478-6	Sequence 6, Appli	
	m	825.2	76.4	1154	4	US-09-484-970B-81	Sequence 81, Appl	
	4	237.4	22.0	873	m	US-09-006-783A-4	4	
	Ŋ	183.8	17.0	1902	(7	US-09-258-257-1	7	
	ø	183.8	17.0	1902	N	-60	i <b></b> i	
	7	183.8	17.0	1902	٣	US-08-569-721A-1	i	
	80	183.8	17.0	1902	٣	US-08-751-230-1	ii	
	σ	183.8	17.0	1902	ო	US-09-499-082-1	H	
	10	183.8	17.0	1902	٣	US-09-258-372-1	· -:	
	11	183.8	17.0	2061	~	US-09-258-371-9	٥,	
	12	183.8	17.0	2061	m	US-08-751-230-9	6	
	13	183.8	17.0	2061	٣	US-09-499-082-9	6	
	14	183.8	17.0	2061	m	US-09-258-372-9	ď	
	15	182.2	16.9	2061	ო	US-09-006-783A-2	7	
	16	182.2	16.9	2061	4	US-09-159-871-1	7	
	17	174.4	16.1	633	m	US-09-006-783A-6	9	
	18	92.6	8.9	678	m	US-09-195-286-3	6	
	19	95.6	8.9	669	ო	US-09-195-286-2	7	
	20	91.6	8.5	1864	4	US-09-620-312D-435	435	
	21	83.6	7.7	451	4	US-09-370-838-146	146,	
υ	22	•	6.7	7218	Н	US-08-232-463-14	14, 7	
	23	50.6	4.7	860	-	US-07-847-010-18	18,	
υ	24	49	4.5	593	ო	US-09-385-982-262	262,	
	25	46.8	4.3	6124	4	US-08-213-419B-3	3, Ar	
	56	46.2	4.3	1189	-	US-07-781-034-4	4	
	27	46.2	4.3	1189	S	PCT-US92-08328-4	4	

Sequence 13, Appl	Sequence 1, Appli	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 1, Appli	Sequence 3, Appli	Sequence 124, App	Sequence 89, Appl	Sequence 3, Appli	Sequence 251, App	Sequence 12, Appl	Sequence 11, Appl	Patent No. 5198345				
US-08-487-826B-13	US-08-916-421B-1	US-09-852-067-1	US-08-728-323A-1	US-09-298-568-1	US-09-410-399-1	US-08-770-379-20	US-08-757-669A-20	US-09-230-371A-20	US-08-665-716-1	US-09-208-742-3	US-09-489-847-124	US-09-489-847-89	US-09-130-491-3	US-09-385-982-251	US-08-956-307B-12	US-08-956-307B-11	5198345-16
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45.8	45.8	43.8	43.8	43.8	43.8	43.8	43.8	43.8	43.4	43.2	43	43	43	42.8	42.8	42.8	42.8
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

Sequence 7, Application US/09601478
; Sequence 7, Application US/09601478
; Patent No. 6403785
; GENERAL INFORMATION:
; APPLICANT: Ostuda Pharmaceutical Co., Ltd.
; TITLE OF INVENTION:
; FILE REFERENCE: Q60193
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US/09/601,478
; PRIOR APPLICATION NUMBER: UP H10-134679
; PRIOR APPLICATION NUMBER: UP H10-73234
; PRIOR FILING DATE: 1998-03-05
; PRIOR FILING DATE: 1998-03-05
; PRIOR FILING DATE: 1998-03-05
; RIOR PILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE PLANCE DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 11 OTHER INFORMATION: human embryonic brain cDNA library NAME/KEY: CDS LOCATION: (92)..(931) TYPE: DNA ORGANISM: Homo sapiens LENGTH: 1078 US-09-601-478-7 US-09-601-478-7 SEQ ID NO 7 FEATURE:

Gaps ö 96.9%; Score 1046; DB 4; Length 1078; 99.5%; Pred. No. 4.4e-264; 1ive 0; Mismatches 5; Indels 0 Best Local Similarity 99.5 Matches 1049; Conservative Query Match

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84	120	144	180	204	240	264
25 GCGGCCGCGGCCGGTGCATGTGCGGCTGCTGCAATGCCGAGGGCGGCGGCGCGCGC	61 CGGCAGGATGTTAGGGCAGCAGCAGCAACAACTGTACTCGTCGGCTGCGCTCCTGACCGG 120	85 CGGCAGGATGTTAGGGCAGCAGCAGCACCACTGTTGTCTCGTCGGCCGCGCTCCTGACCGG 144	121 GGAGCGGAGCCGGCTGCTCACCTGCTACGTGCAGACTACCTTGAGTGCGTGGAGTCGCT 180	145 GGAGCGGAGCCGGCTCGCTTCTTTTTTTTTTTTTTTTTT	181 GCCCCACGACATGCAGGAGGAGGTGTCTGTGCTGCGAGAGCTGGACAAATATCAAGA 240	205 GCCCCACGACATGCAGAAGAACGTGTCTGTGCTGCAGAGAGACGACAACAAATATCAAGA 264
25	61	85	121	145	181	205
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241 AACGTTAAAGGAAATTGATGATGTCTACGAAAAATATAAGAAGAAGATGATTTAAACCA 300

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SEQ ID NO 6
LENGTH: 840
TYPE: DNA
ORGANISM: HOMO B
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  TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAT
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                                                                  TGAAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAT
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TITLE OF INVENTION: Human TSC403 gene and hr
FILE REFERENCE: G60193
CURRENT APPLICATION NUMBER: US/09/601,478
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: JP H10-73234
PRIOR FILING DATE: 1998-03-05
PRIOR PELING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
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                                                                                   Length 840;
                                                                                                                     Indels
             FEATURE: OTHER INFORMATION: human embryonic brain cDNA library
                                                                                Score 838.4; DB 4;
Pred. No. 7.9e-210;
0; Mismatches 1;
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US-03-444-970B-81
; Sequence 81, Application US/09484970B
; Patent No. 6426186
                                                                                   77.6%;
                                                                                                    Best Local Similarity 99.9
Matches 839; Conservative
sapiens
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1081 ATAAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTAC 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gudkov, Andrey V
APPLICANT: Garkavstev, Igor
TITLE OF INVENTION: Pathway
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 873;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPILING DATE: US/09/006,783A
FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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0; Mismatches 291;
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Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09006783A Patent No. 6297366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: No. 6297366nan, Kevin
REGISTRATION NUMBER: 35,303
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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59.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 base pairs
TYPE: nucleic acid
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Matches 462; Conserv
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Pred. No. 2.7e-206;
                       APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Wichael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
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Best Local Similarity 97.9%;
Matches 836; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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LOCATION: 17-37
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LENGTH: 1154
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57.0%; Pred. No. 2.2e-38;
tive 0; Mismatches 267;
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                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  REGISTRATION NUMBER: 37,047
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028
TELECOMMUNICATION: (650) 854-7400
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (650) 854-7400
TELEPAX: (650) 854-8275
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/258,257
FILING DATE:
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
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Patent No. 5965398
GENERAL INFORMATION:
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<u>AGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA</u>686
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                                       509 TCTTCAAGAA--GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG 566
                                                                           335 CCAACAGCAAGCGCTCACGGCGGCAGCGCAACAACGAGAACCGTGAGAACGCGTCCAGCA 394
                                                                                                               567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA 626
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 275 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 1404
CITY: Alexandria STREE: Virginia
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Patent No. 6037121
GENERAL INFORMATION:
APPLICANT: GARKAVISEV, IGOR
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: SUPPRESSOR GENE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUINB, DOADE, Swecker & M.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LeBlie A:
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear _ MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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COUNTRY: United States
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                                                                                                                                                 APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol., Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING!
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNE, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                     STREET: Burns, Doane, Swecker & Mathis STREET: 699 Prince Street CITY: Alexandria STATE: VA COUNTRY: USA ZIP.
695 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 725
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-144
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
                                                                   5-09-258-371-1
Sequence 1, Application US/09258371
Patent No. 5986078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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ilarity 57.0%;
Conservative (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                               GENERAL INFORMATION:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-09-258-371-1
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Best Local S
Matches 394
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GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTTTCACTTACCT 806
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                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONTRARE: Patentil Nelease #1.0, Version #1.30
SUGNARS: Patentil Nelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: MOOJ, Lealie A.
REGISTRATION NUMBER: 37.047
REGISTRATION NUMBER: 37.047
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Pred. No. 2.2e-38;
0; Mismatches 267;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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Best Local Similarity 57.0%;
Matches 394; Conservative
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                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-751-230-1
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                                                                                                                                                         Gaps
                                                                                                                                                  30;
                                                                                            Length 1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATGGAGTTACACTCACAGTGTTTCCAAGATC---------
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                                                                                      Score 183.8; DB 3;
Pred. No. 2.2e-38;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Burns, Doane, Swecker & Mathis
699 Prince Street
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APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING
TITLE OF INVENTION: SUPPRESSOR GENE INGI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathic
STREET: 699 Prince Street
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; Sequence 1, Application US/08751230
; Patent No. 6117633
                                                                                      Query Match
Best Local Similarity 57.0%;
Matches 394; Conservative
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STATE: VA
COUNTRY: USA
ZIP: 22313-1404
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LOCATION:
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US-08-569-721A-1
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                                                                                                                                                                                                                                                                                                                                                                             335 CCAACAGCAAGGGGTCACGGCGGCAGCGCAACAACGAGAACCGTGAGAACGCGTCCAGCA 394
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                                         ENCODING THE TUMOR INE INGI
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Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Riabowol, Karl
TILLE OF INVENTION: DNA SEQUENCE ENCOD:
TITLE OF INVENTION: SUPPRESSOR GENE INV
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEB: BURNS, Doane, Swecker & M.
STREET: 699 Prince Street
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
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ZIP: 22313-1404
COMPUTER READABLE FORM:
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US-09-258-372-1
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Helbing, Caren C.
APPLICANT: Riabowol, Karl
APPLICANT: Johnston, Randall N.
APPLICANT: Garkavtesov, Igor
ITILE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/499,082
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T: 699 Prince Street
Alexandria
                                                                                                                                                                ACAAAGCCCTGGAGAATCCAAAAAAGAGAG 725
                                                                                                                           867 ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
PILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
                                                                                                                                                                                                                                                                     Sequence 1, Application US/09499082
Patent No. 6143522
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REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 02E
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1
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LENGTH: 1902 base pairs
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STRANDEDNESS: double
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Best Local Similarity
Matches 394; Conserv
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US-09-499-082-1
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US-09-499-082-1
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                                                                                                                                                                                                                                                     ENCODING THE TUMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/258,371
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Pred. No. 2.3e-38;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATGGAGTTACACTCACAGTGTTTCCAAGATC-----
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: _699 Prince Street
                                                       Sequence 9, Application US/09258371
Patent No. 5986078
GENERAL INFORMATION:
APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: SUPPRESSOR GENE ING1
TITLE OF INVENTION: SUPPRESSOR GENE ING1
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-954-7400
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
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Best Local Similarity 57.0
Matches 394; Conservative
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STRANDEDNESS: double
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-09-258-371-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
RESULT 11
US-09-258-371-9
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17.0%; Score 183.8; DB 3;
Best Local Similarity 57.0%; Pred. No. 2.2e-38;
Matches 394; Conservative 0; Mismatches 267;
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                                                                                                                                                 028722-144
                                        ATTORNEI/ACCENTRATION INVARER: 37,047
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287;
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELESPHONE: 415-854-7400
TELESPAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1902 base pairs
LENGTH: 1902 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
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US-09-258-372-1
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                                                                                                          Gaps
                                                                                                        30;
                                                                  Length 2061;
                                                                Score 183.8; DB 3; Length 2
Pred. No. 2.3e-38;
0; Mismatches 267; Indels
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APPLICANT: Helbing, Caren C.
APPLICANT: Halbing, Karl
APPLICANT: Rabowol, Karl
APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
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Patent No. 6143522
                                                                Query Match
Best Local Similarity 57.0%;
Matches 394; Conservative
        16..900
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STATE: VA
COUNTRY: USA
        LOCATION:
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US-09-499-082-9
            US-08-751-230-9
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                                                                                                                                                                                   614 AGAAGAAGAAGCGCTCCAAGGCCAAGGCGAAGGCGAGAGGCGTCCCCTGCCGACCTCCCCA
                                                            567 CAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCAA
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MEDIUM TYPE: Floppy disk
COMPUTER: PROPPY disk
COMPUTER: PROPPY disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751,230
FILING DATE: 15-NOV-1996
CLASSIFICATION 1514
PRIOR APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
ATTOMEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Garkavtsev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-854-7400
TELEFAX: 415-854-8275
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA
FEATURE:
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                             747 GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 183.8; DB 3;
Pred. No. 2.3e-38;
0; Mismatches 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                  854 ACAAAGCCCTGGAGAAATCCAAAAAAGAGAG 884
                                                                                                                                                                                                                                                  867 ACAAAAGTACTGAAAAGACAAAAAAGGATAG 897
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application US/09258372
Patent No. 6238918
GENERAL INFORMATION:
APPLICANT: Garavtsev, Igor
TITLE OF INVENTION: DNA SEQUENCE ENCODING 1
TITLE OF INVENTION: SUPPRESSOR GENE ING1
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/751,230
FLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mooi, Leslie A.
REGISTRATION NUMBER: 37,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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57.0%;
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Best Local Similarity 57.0
Matches 394; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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ZIP: 22313-1404
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, LOCATION:
US-09-258-372-9
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US-09-258-372-9
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                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2.3e-38;
0; Mismatches 267;
                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
FILING DATE:
CLASSIFICATION NUMBER: US/09/499,082
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569721
TELECOMMUNICATION NUMBER: 37,047
REFERENCE/DOCKET NUMBER: 028722-148
TELECOMMUNICATION INFORMATION:
TELECHONE: 650-854-7400
                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COSTWARE: Patentin Policial
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57.0%;
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 57.09
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16..900
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; LOCATION:
US-09-499-082-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.9%; Score 182.2; DB 3;
56.9%; Pred. No. 6.1e-38;
tive 0; Mismatches 268;
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NAME: No. 6297366nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAR: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.9
Matches 393; Conservative
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LOCATION:
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APPLICANT: Gudkov, Andrey V
APPLICANT: Garkavstev, Igor
APPLICANT: Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
TITLE OF INVENTION: Pathway
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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FILING DATE: 15-JAN-1998
CLASSIFICATION: 435
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Patent No. 6297366
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CORRESPONDENCE ADDRESS:
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-09-006-783A-2
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: January 12, 2004, 16:38:42; Search time 2229 Seconds (without alignments) 11776.058 Million cell updates/sec Title: US-09-513-365A-2 Perfect score: 1080 Sequence: 1 geogcogotgocatgaaaaaaaaaaaaaaa 1080	able: IDENTITY NUC Gapop 10.0, Gapext 1.0 22781392 seqs, 12152238056 residues ber of hits satisfying chosen parameters: 45562784		Database : EST:*  1: em_estba:* 2: em_esthum:* 3: em_estin:* 4: em_estin:* 5: em_estov:* 6: em_estov:* 7: em_estro:* 8: em_htc:* 9: gb_estr:* 11: gb_htc:* 12: qb_est2:*		25: em_gas_phg:* 26: em_gas_phg:* 27: em_gas_vrl:* 28: gb_gas1:* 29: gb_gas2:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Result Query No. Score Match Length DB ID Description  1 828 76.7 2643 11 AK048800 AK048800 Mus muscu 2 827.6 76.6 2812 11 AK083144 AK083144 Mus muscu 3 812.8 75.3 1464 11 AK012716 AK012716 Mus muscu 4 747.8 69.2 912 13 BQ277444 AGENCOURT

REFERENCE AUTHORS

MEDLINE PUBMED REFERENCE

JOURNAL

TITLE

AUTHORS

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/codon_start=1
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QTUTQMLETUSNRARQWELHSQCRQDPAESRRASDKSKMDSSQERRSREPRRQRYSE
STDLCHMTNOI IDDODOPPERGKSAKKKKRSKAKQEREASPVEFAIDPNETYCLC
NQVSYGBMIGCDNEQCPIEWPHFSCVSLTYKFKGKWYCPKCRGDNEKTMDKSTEKTKK
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Pred. No. 1.2e-94;
0; Mismatches 118; Indels
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476._.1321
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Best Local Similarity 88.3
Matches 933; Conservative
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Fletcher,C., Fultta,M., Garibold,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Stoch,K.F., Suzuki,H.,
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Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
and Hayashizaki,Y.
Nuture 409 (6821), 685-690 (2001)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
E (bases I to 2643)
Adachi, J. Aizawa, K., Akimura, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiracka, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Saitoh, R., Saitoh, R., Sakai, K., Sakazume, N.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Muramatsu, M., and Hayashizaki, Y., Yatunishi, A.,
Muramatsu, M., and Hayashizaki, Y.,
Direct Submission
Olivect Submission
All Submitted (16-JUL-2011) Yoshhinde Hayashizaki, The Institute of Physical and Chemical Research (RIKEN) Laboratory for Genome Exploration Research Group, RIKEN Genome, Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-reseggscriken.go.jp,
REX:BLTEN YOKOHAM SECTIKEN GEOTERS (188-9522, 188-8518)
ANN HANN HANN SECTIKEN GEOTERS (188-9522, 188-8518)
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Please visit our web site for further details.
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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TITLE JOURNAL MEDLINE PUBMED

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Group Phase I E II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

I Nature 420, 563-573 (2002)

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E Adachl, J., Aizawa, K., Akimura, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hirim, Y., Kondo, S., Konno, H., Kowai, J., Kasukawa, T., Katoh, H., Kawai, J., Kondo, S., Konno, H., Kowai, J., Kojima, Y., Kondo, S., Konno, H., Kowai, M., Ohana, M., Ohasto, N., Ohasto, N., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sakazume, N., Sakai, C., Sakai, K., Sakazume, N., Sakazume
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
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Nature 409 (6821), 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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|db_xref="taxon:10090"
|clone="C630016P10"
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/strain="C57BL/6J"
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      .009 ACCGAAAGAAAAGAGATCCAAGTCCGCCAAGAAGAAGAAGCGCTCCAAGGCCAAGCAGGA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GITTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCA 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                               GTGCAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAGACAAAAAGGATAG
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2812 bp mRNA linear HTC 05-DEC-Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630016P10 product:inhibitor of growth family, member 1-like, full insert sequence:
                                                                                                                                                                                           718 CAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGAATG
                                                                                                                                                                                                                                                                                                                       GTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCCAAA
                                                                    658 AAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATG
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                               Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810011MG product:inhibitor of growth family, member 1-like, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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  GTTTGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTAATCA
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Mus musculus (botae mouse)
Eukaryota; Metazoa; Chordata
Mammalia; Eutheria; Rodentia
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Codon start=1

/protein id="BAC38783.1"
/brotein id="BAC380287"
/brotein id="BAC380287"
/translation="MiGQQQQQQLYSSAALLTGERSRLLSCYVQDYLECVESLPHDMQ
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QIYQMLELLVBRRARQMELHSQCFQDPAESERASDKSWMDSSQPERSSRRPRRQRTSE
SRDLCHMTNGIDDCDQPPKERSKGAKKKKRSKRAKQEREASPVERAIDPNEPTYCLC
NQVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKK
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469 GGCGGCAGGATGTTAGGGCAGCAGCAGCAGCAGCTGTACTCGTCGGCCGCCCCCCCTC 528
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/ organism="Mus musculus"
/ organism="Mus musculus"
/ mol_trype="mana"
/ strain="CSTBL/60"
/ db_xref="FANTOM DB:2810011M06"
/ db_xref="Raxon:10090"
/ clone="2810011M06"
/ tissue type="whole body"
/ clone="ib="RIKEN full-length enriched mouse cDNA library"
/ dev_stage="10, 11 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Genomic Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGGATCCAAGAGCTTTTTTTTTTTTTTTTTTNN 3], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIREN), inboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:Genome-res@gsc.riken.go.jp, NWE.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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McCray Lab
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E 1 (bases 1 to 912)

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Preparation: Michael Brownstein (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
High quality sequence stops: 587.
                                                                            AGENCOURT 6738254 NIH_MGC_127 Homo sapiens cDNA clone IMAGE:5810745
5', mRNA Sequence.
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Normalization and subtraction: two approaches to facilitate gene
                      TGCGTGGAGTCGCTCCCACGACGACGACGAGGAACGTGTCTGTGCTGCGGAGAGCTGGAC
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CAAGAATTGGGAGATGAAAAAAAAAAAAGATTGTTACACAAATGCTCGAATTGGTGGAAAAT
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                                                                               CGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGA
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97044477
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937

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BG184056 798 bp mRNA linear EST 21-APR-2001
RST2972 Athersys RAGE Library Homo sapiens CDNA, mRNA sequence.
BG184056
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Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                                                        195 GAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAAGGGTT 136
                                                                                                                                         315 GAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTTCACTTACCTATAAACCAAAG 256
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                                                                                                                                                                                                                                                                                                                                                                                                                135 ATTTGTCTTTTATATATTCGTTTGCTTTCAGAAATGTTTTAGGGTAAATGCATAAGAC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                     GGGAAATGGTATTGCCCAAAGTGCAGGGAGATAATGAGAAAAAAAGTACT
           GAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAAT
                                                                                               GAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAG
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Tel: 216 431 9900
Fax: 216 361 9596
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Scott J. Cain
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BG184056/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cells"
/dev_stage="Adult"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/clone lib="UL-CF-EN1"
/note="Crgan: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
Ul-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:991-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligomuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is
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2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 316 4866
Fax: 319 316 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
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6hr to LPS 24h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCGTAAT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 ATTAATAGTCAAGAATTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     458 AGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518 AGACCCCGCAGCGGACCAGTGAAAGCCCGTGATTTATGTCACATGGCAAATGGGATT
                                                                                                                                                                                                                                                                                                                     1. 735
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EM1-acs-d-05-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
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_161 c 114 g
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                               (www.openbiosystems.com).
Seg primer: M13 FORWARD
POLYA=Yes.
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Best Local Similarity
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/ciouser.ryades.3941035
/tissue tynades.3941031
/cell line="MGC3"
/lab host="DH10B (phage-resistant)"
/clone lib="NH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lung; Vector: poTB7; Site_1: XhoI; Site_2: Secolif or printing for average insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies)."
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                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM794 row: a column: 16
High quality sequence stop: 769.
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                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Eutheria; Primates; Catarrhini; Hominidae; Homo
1 to 793)
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Pred. No. 9.1e-80;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3941655"
                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.8%;
Best Local Similarity 98.9%;
Matches 747; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                         Gaps
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                      DB 10; Length 798;
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                    Score 727.6; DB 10;
Pred. No. 7.7e-82;
0; Mismatches 4;
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                      Query Match
Best Local Similarity 98.9%;
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521 AAAGAT(	8 8 8 8 8 8	8 6 8 6 8 6 8	8 8 8 8 8 8	COSSE BOSSE	DOEP VERY KEYN KEYN SOUG OG T. T. T.
DD  OY  OY  OY  OY  OY  OY  OY  OY  OY		720 ACCAAGTGTCTTATGGGGAGATGATAGGATGTGAC 754	DS EST.  Homo sapiens (human)  NISM Homo sapiens  Homo sapiens  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele  Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.  NCE 1 (bases 1 to 77 and 1 to 10	DNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAMI1661 row: n column: 13 High quality sequence stop: 775. Location/Qualifiers 1. 778 Source /organism="Homo sapiens" /mol type="mRNA" /db xref="taxon:9666" /tissue type="hippocampus" /lab_host="hippocampus"	OUNT 237 s y Match Local Similari hes 718; Cons

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/dev stage="fetal and adult"
//dev stage="fetal and adult"
//lab_host="DH10B (Life Technologies) (T1 phage resistant)"
//clone_lib="UUI-E-EJ1"
//clone_lib="UUI-E-EJ1"
//note="Organ: eye, Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ1 is a subtracted =DNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAACGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                                                                                                                                                                                                                                                                                                                    BM682789 675 bp mRNA linear EST 27-FEB-2002
UI-E-EJI-ajf-g-22-0-UI.sl UI-E-EJ1 Homo sapiens cDNA clone
UI-E-EJ1-ajf-g-22-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 315 826
Fax: 319 315 826
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa CIONE Distribution: Researchers may obtain clones from Research
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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/mol_type="mRNA"
/db_xref="ttansor"
/db_xref="ttansor"
/db_xref="ttansor"
/clone="U1-ExD1-ajf-g-22-0-U1"
/tissue_type="fetal eyes, lens, eye anterior segment,
optio_nerve, retina, Retina Foveal and Macular, RPE and
                      956 TCGTTTGCTTTCAGAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAAT
                                                                                                        B96 AGAAGATCGAGGTAGTAAAGGCCCATCCACATTTTAAAGGGTTATTTGTCTTTTATATAT
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Coordinated Laboratory for Computational Genomics
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Seg primer: M13 Forward
POLYA=Yes.
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/note="See 'Creation of Genome-wide Protein Expression
/note using Random Activation of Gene Expression
Libraries using Random Activation of Gene Expression
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method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%; Score 680.8; DB 10; Length 919; 95.1%; Pred. No. 4.9e-76; ive 0; Mismatches 30; Indels 11;
                                                              Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
                                                                                                                                                                      High quality sequence stop: 439.
Location/Qualifiers
                                              Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                    . .919
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                      11329013
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hes 788;
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ORIGIN
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/CLORE 1103 "OLIS-EDJI"
// Model 1103 "OLIS-EDJI"
// Modified polylinker; Site_1: ECOR I; Site_2: Not I;
UI-E-EJI is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA;
iles, CGATTAGCGA; eye anterior segment, AATGCCGCA;
optic nerve, CCATTAGCG; retina, CGCGG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
                                                                                                                                                          /dev stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone lib="UI-E-EJ1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 GTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGGAAAGATGGATTCCAGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACCAGAAAGATCTTCAAGAAGACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCC 616
                      1 (bases 1 to 664)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="UI-E-EJI-ajf-g-22-0-UI"
/tissue type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTTACACAAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAAAATGGGCCACAGG
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      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 663; DB 12;
Pred. No. 9.8e-74;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                  Genome Rés. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.4%;
Best Local Similarity 99.8%;
Matches 663; Conservative
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                                                                                      discovery
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ORIGIN
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AUTHORS
TITLE
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MEDLINE
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COMMENT
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                                                                                                                                                                                                                                                                                                      616
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Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-EJI
TAG_TISSUE=Foveal and Macular Retina
TAG_ESC=GTCC"
118 c 110 g 253 t
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                         GTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACCGTGTTTCCAAGATCCTGCTGAA
                                                                                                                                                                                                                                                                                                                                                                 AGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCACCCAACCAGAAAGATCTTCAAGA
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                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                    DB 12; Length 675;
                                                                                                                                                                                Score 671.8; DB 12; Length
Pred. No. 7.8e-75;
0; Mismatches 2; Indels
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ilarity 99.7%;
Conservative
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                                                                                                                       164
                                                                                                                                                                                                                   673;
                                                                                                                                                                                Query Match
Best Local S:
Matches 673,
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                       BASE COUNT
ORIGIN
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/tissue_type="cochie"
/dev stage="16-22 week fetus"
/dev stage="16
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BI091047 GI:14509377
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Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
761: 617 732 7980
Fax: 617 738 6996
Email: ccmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6327 row. G column: 7
Seq primer: T7 primer.
Location/Qualifiers
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1 (bases 1 to 653)

1 (bases 1 to 653)

2 (An estraton, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.

1 solation of novel and known genes from a human fetal cochlear cDNA ilbrary using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
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df121d04.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
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AAGTCAGCAAAGAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTT
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/mol_type="mRNA"
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us-09-513-365a-2.rst

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imag-llh.gov
Plate: LLAM11675 row: f column: 18
High quality sequence stop: 700.
Location/Qualifiers
                                                                                                                                                                                                                                                                                       BI460319 708 bp mRNA linear EST 21-AUG-2001
603201967F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5267729 5',
                                                                       GTACTGAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAA 113
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      232 CAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGAGATAATGAGAAAACAATGGACAAAA 173
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Buthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 708)
MIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
Unpublished
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/db_xref="texon:9606"
/clone="lMAGE:5267729"
/lab_hos=="DHIOB"
/clone lib="NIH_MGC 97"
/note="Organ: testis; Vector: pBluescriptR (modified
                                                                                                                                                                      993 AAGACTATGCAATAATTTTTAATCATTAGTATTAATGGTGTATTAAAAGTTG 1044
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Pred. No. 9.2e-67;
0; Mismatches 6; Indels
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/organism="Homo sapiens"
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al Similarity 98.9%;
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                                                                                                                           /cell_line="MGC36"
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/clonellib="NHH_MGC_10"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 kb. Library prepared by Life
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/clone="IMAGE:4996593"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
GTTAGGGCAGCAGCAGCAGCACTGTACTCGTCGGCGGCGCTCCTGACCGGGGAGCGGAG
                                      CGGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGA
                                                                                               CATGCAGAGGAACGTGTCTGTGCTGCGAGAGCTGGACAACAAAATATCAAGAAACGTTAAA
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                         CCGGCTGCTCACCTGCTACGTGCAGGACTACCTTGAGTGCGTGGGAGTCGCTGCCCCACGA
                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)
TONA Library Preparation: Catherine Lee, Endocrine Pancreas
Consortium
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High quality sequence stop: 560.
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/db_xref="taxon:10090"
/clone="IMAGE:6430926"
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/clone lib="NIH MGC 137"
/clone lib="NIH MGC 137"
/clone lib="Organ: pancreas; Vector: pSPORTI; Site 1: Sall;
Site 2: Not!; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 NI-MMSI, Amplified Melton mouse
islets 1 MISI-A, and Kaestner ngn3 wt. Clones rearrayed in
the laboratory of K. Kaestner (University of Pennsylvania
). Note: this is a NIH MGC Library."
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Matches 681; Conservative
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Location/Qualifiers 68..910 /\*tag= a /product= "Tumour suppressor homologue protein, p33ING2" Tumour suppressor; p471NG3; cell proliferation; cellular aging; p331NG2; anchorage dependence; apoptosis; tumour; cancer; gene therapy; ds. Tumour suppressor homologue protein, p33ING2 DNA ALIGNMENTS (USSH ) US DEPT HEALTH & HUMAN SERVICES. AAH03733 AAH28480 AAH28481 ABQ50058 ABQ50059 ABQ50060 ABQ50061 ABQ77429 AAT23370 AAK52101 ABL15055 ABA08933 AAF90402 AAF90399 AAL37089 ABX60077 AAD46126 ABK86976 AAA53789 AAX28688 **ABQ54665** AAD12783 standard; DNA; 1080 BP 09-FEB-2001; 2001WO-US04425 09-FEB-2000; 2000US-0181292 23-OCT-2001 (first entry) Nagashima M; WO200159114-A2 Unidentified 16-AUG-2001 Harris CC, 236 236 197.2 183.8 183.8 183.8 1183.8 1183.8 183 182.4 182.2 175 142.6 125.8 125.8 124.6 124.6 102 101.4 98.8 97 183.4 AAD12783; AAD12783 Tumour suppressor Human INGIL encodi Human INGIL encodi Human tumour suppr Human bone remodel Human secreted pro Human tumour suppr Murine P371NG1 cod January 12, 2004, 16:38:42 ; Search time 334 Seconds (without alignments) 8728.722 Million cell updates/sec Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. N Geneseq 19Jun03:\*

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25: /SIDSI/gcgdata/geneseqfy-emeseqn-embl/NA2003.DAT:\* Description GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. Total number of hits satisfying chosen parameters: 2552756 seqs, 1349719017 residues SUMMARIES Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries nucleic search, using sw model AAZ08596 AAZ47473 AAZ47473 ABS70424 AAC28459 AAZ47474 AAD12783 IDENTITY NUC Gapop 10.0 , Gapext 1.0 B seq length: 0 seq length: 200000000 US-09-513-365A-2 1080 Length DB 1080 1078 840 1153 1154 346 325 Query Match 100.0

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                                                                                                                                          The present sequence is a DNA encoding tumour suppressor homologue protein, p31NG2 which is homologous to human tumour suppressor protein, p47NG3. The tumour suppressors of the invention are involved in the regulation of cell proliferation and in the control of cellular aging, anchorage dependence and apoptosis. The tumour suppressor protein, p47NG3, nucleic exide encoding it and antibodies against it are useful for diagnosis, prevention and treatment of tumours and cancers. The p471NG3 DNA is also used in gene therapy.
                                                                                                                                                              protein,
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0; Mismatches 0;
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                     2001-488975/53
                   WPI; 2001-488975/
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    The present sequence represents the human tumour suppressor gene INGIL. The present invention also describes the human gene TSC403 expressed specifically in normal lung tissue. TSC403 is useful in the diagnosis, investigation and treatment of cancers in which it is overexpressed, including cancer of the lung, breast, fallopian tube, oesophagus, colon, thyroid, parotid gland, bladder, ovary or pancreas. INGIL is useful in the investigation of cell proliferation, aging and apoptosis and the pathology of cancer, the diagnosis and treatment of cancer such as cancer of the colon, stomach, oesophagus or fallopian tube, and the screening of candidate drugs for the treatment of such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lung-specific gene TSC430 overexpressed in cancer tissue, used for treatment of, e.g. colon tumour
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apoptosis and the pathology of cancer, the diagnosis and treatment of cancer such as cancer of the colon, stomach, oesophagus or fallopian tube, and the screening of candidate drugs for the treatment of such
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96.9%; Score 1046; DB 20; Length 1078;
Best Local Similarity 99.5%; Pred. No. 4.9e-229;
Matches 1049; Conservative 0; Mismatches 5; Indels 0;
                                                               Sequence 1078 BP; 356 A; 206 C; 280 G; 236 T; 0 other;
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/note= "Tumour suppressor protein"

TUSUP

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This sequence encodes the human tumour suppressor (TUSUP) protein. The TUSUP sequence was identified from a human lung cDNA library. The protein is 240 amino acids in length and has one potential cAMP and CGMP dependent protein kinase phosphorylation site, nine potential protein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation sites, and one potential similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal tracts or of the immune system. Agonists of the TUSUP protein can be used to raise TUSUP specific antibodies and to screen for specific binding agents and potential therapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of
                                                                                                                                                                                                                                                                                           New human tumour suppressor protein for treating cancer, particularly reproductive and gastrointestinal tracts or immune system
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                                                                                                         Gaps
                                                                   Length 1153;
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                                                                                                         IndelB
                                Sequence 1153 BP; 367 A; 215 C; 285 G; 265 T; 21 other;
                                                                 Score 825.2; DB 21;
Pred. No. 1.3e-178;
0; Mismatches 18; I
diagnostic probes and primers.
                                                                      76.4%;
97.9%;
                                                                   Query Match
Best Local Similarity 97.9
Matches 836; Conservative
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Tumour suppressor protein; TUSUP; human; cancer; treat; prevent; reproductive tract; gastrointestinal tract; immune system; ss.

Location/Qualifiers 277..999

Key

sapiens

Human tumour suppressor (TUSUP) nucleotide sequence.

(first entry)

14-MAR-2000

L H X S X & & X E X D X Y X I I

AAZ47473;

BP

AAZ47473 standard; cDNA; 1153

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Gaps

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Tectgaaagtgaacgagcctcagataaagcaaagatggattccagccaaccagaaagatc
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                                                                                                                                             AAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCTCCAGAG
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                                                                                           GCTGCGAGAGCTGGACAACAATATCAAGAAACGTTAAAGGAAATTGATGATGTCTACGA
                                                                                                                  301 Gercegacercecegarecreserececaaacerraaagaaarraarearerraea
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                                        Length 1154;
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                                                                Indels
                367 A; 216 C; 285 G; 265 T; 21 other;
                                      24;
                                      Score 825.2; DB 24;
Pred. No. 1.3e-178;
0; Mismatches 18;
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                                      76.4%;
ilarity 97.9%;
Conservative
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                                                                                                        AAGTACTGAAAAGACAAAAAAGGATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTA
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                                                                                                                                                                                                                                                                                                                TCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATG
                                                                                         TGACAATGAACAGTGCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAA
                                                                                                                                             ACCAAAGGGGAAATGGTATTGCCCAAAGTGCAGGGGGGGAGATAATGAGAAAACAATGGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodelling and osteoporosis. The invention is used to diagnose disorders associated with bone remodelling or osteoporosis, ABS70344-ABS70512 represent human bone remodelling genes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A combination of polynucleotides which are co-expressed with genes known to be involved in bone remodeling and osteoporosis are useful an array for the diagnosis of bone remodeling and osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bone remodelling; osteoporosis; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Column 239-242; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Walker MG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA; 1154
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301 THNNTGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCCA 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and the contract of the contract o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                              Human, S' EST; expressed sequence tag, secreted protein; cDNA isolation; gene therapy, chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ATTGATGATGTCTACGAAAATATAAGAAGAAGATGATTTAAACCAGAAGAAACGTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                             Human secreted protein 5' EST, SEQ ID NO: 32534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 32534; 71pp + CD-ROM; English.
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99.1%;
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                             06-OCT-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-1999;
                                                                                                                                                                                                              Homo sapiens
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This sequence was used to determine the sequence of the human tumour suppressor protein (TUSUP) see AAY52199. The TUSUP protein is 240 amino acids in length and has one potential cAMP and GGMP dependent protein kinase phosphorylation sites, ince potential protein kinase phosphorylation sites, five potential casein kinase phosphorylation sites, and one potential tyrosine kinase phosphorylation site. TUSUP has structural and chemical similarity to p33. TUSUP can be used to treat or prevent cancer, particularly of the reproductive or gastrointestinal used to raise TUSUP specific antibodies and to screen for specific binding agents and potential herapeutic agents. The TUSUP nucleotide sequence can be used in gene therapy and as a source of diagnostic probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 TTATGGGGAGATGATAGGATGTGACATGAACAGTGTCCAATTGAATGGTTTCACTTTTC 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human tumour suppressor protein for treating cancer, particularly of reproductive and gastrointestinal tracts or immune system -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 GTAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATATAATTCGTTTGCTTTTCAG
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                                                                                                                                                                                                                                                                                    Tumour suppressor protein, TUSUP, human; cancer, treat, prevent, reproductive tract; gastrointestinal tract; immune system; ss.
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                                                                                                                                                                                                                suppressor (TUSUP) fragment nucleotide sequence.
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100.0%; Pred. No. 1.3e-64;
tive 0; Mismatches 0;
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AAZ47474 standard; cDNA; 325
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Best Local Similarity 100.
Matches 325; Conservative
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   AAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTAGTATTAATG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head and eck cancers and chromosomal location of the ING1 placed it cancers cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 mor significant variations in its expression suggesting that ING1 was not a useful gene to study in cancer eriology. However, alternative initiation exons of the ing1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting nucleic acid encoding exon 1b of ingl, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                   AAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCGTTAGTATTAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             having
                                                                                                                                                                                                                                                                            p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene, each having their own promoter have been discovered.

Expression of one promoter (1a) produces a protein identical to INGI. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to INGI but an additional 104 N-terminal amino acids. The newly discovered protein has been chasigned by 1010 (Wild type: p31NGI) has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37INGI is able to cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grigorian IA;
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/product= P371NG1 polypeptide
                                                           1054
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                           GTGTATTAAAAGTTGTTGTACTTTG
                                                         GTGTATTAAAAGTTGTTGTACTTTG
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                                                                                                                                                                                                                                               Murine P37ING1 coding sequence.
                                                                                                                                                            AAA53790 standard; cDNA; 2817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAAATGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAAGAAATCCAAGTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                             nucleic acid encoding exon 1b of ingl by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ingl or its antisense sequence con identify individuals expressing the oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2817;
           Thus detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 253.6; DB 21; Length
Pred. No. 5.8e-48;
0; Mismatches 289; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2817 BP; 670 A; 711 C; 846 G; 590 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAATGGAGTTACACTCACAGTGTTTCCAAGATCCTGCTGAAA-
proliferation or transformation of those cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACAAAGCCCTGGAGAAGTCCAAGAAAGAGAG 1670
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60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 490; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 studying cancers.
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Gaps

145 264 324

384

505

654

685 774

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Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of tumours. In remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING1 encoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head can exert and encreased and encoded and encoded it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not revealed mutations in ING1 mor significant variations in its expression suggesting that ING3 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting nucleic acid encoding exon 1b of ing1, useful for diagnosing and treating cancer, comprises contacting sample with isolated nucleic acid comprising sequence of exon 1b and detecting hybridized products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression of one promoter (1a) produces a protein identical to 1867. Expression of one promoter (1a) produces a protein identical to 1867. Expression of a second promoter (1b) produces a protein having an identical C-terminal fragment to ING1 but an additional 104 N-terminal amino acids. The newly discovered protein has been designated by 371NG1 wild type: 931871671. p371NG1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p371NG1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon 1b of ing1 by hybridisation with an isolated nucleic acid having the sequence of exon 1b of ing1 or its antisense sequence can identify individuals expressing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oncogenic form of ingl. Novel peptide sequences taken from the 104 N-terminal peptide of p371NG1 can also be used to raise antibodies that can also be used in detection methods for the p31NG1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                p53; tumour; cancer; detection; antibody; hybridisation; exon 1b; ING1; ing1; p331NG1; p371NG1; oncogene; gene therapy; diagnosis; proliferation disorder; transformation; transformed cell; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grigorian IA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 122-123; 134pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gurova KV,
                                        ВР
                                                                                                                                                                     Human P37ING1 coding sequence.
                                        standard; cDNA; 911
                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000WO-US02959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0118941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNII ) UNIV ILLINOIS FOUND
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zeremski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-491278/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAY97244
                                                                                                                                                                                                                                                                                                                                                    WO200046370-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1999;
                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                               19-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gudkov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                        AAA53792
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RESULT 9
                      AAA53792
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-----CTGCTGAAAGTGAACGAGCCTCAGATA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 GGCGCAGCAGGAGGCTGGGCGACACAGTGGGCAACGGCAAGGTTGGCGCGGACAGGCC 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      566 cacacccaaggagagagagagagaccrccaagaagaagaagagccrccaaggccaaggc 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 CCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAAATACAGATTGTTACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTGTGCTGCGAGGCTGGACAACAATATCAAGAAACGTTAAAAGGAAATTGATGATGT
                                                                                                                                                                                                                                                                                                                                                      146 croccroarcegeagarceaceceaaaraccaagaearccroaageageragaeage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u> craccades controles de casas de casas casas de casas de</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 AATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGTGTTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    506 CAACAACGAGAACGCTGAAACGCGTCCAGCAACCACGACCACGACGACGACGCCTCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    715 ATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             775 ATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       835 AAAGTGCAGGGAGATAATGAGAAAAAAAGAGACAAAAGTACTGAAAAAGACAAAAAAGA
                                                                                                                                              145 CTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCTGCCCCACGACATGCAGAACGT
                                                                                                                                                                                                               chandridgaddadricchanceadriccchecchriceachiceadadad
                                                                                                                                                                                                                                                                                                                                                                                                                            CTACGAAAAATATAAGAAAGAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      477 AAGCAAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCCGCAG--GCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 GACCAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626 ecaccacadocercecercecacerceceáreceáreceaneanecadocaderarer
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                                                                            30;
   Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of a human cancer associated antigen.
                                                                            Indels
DB 21;
                                                                        0; Mismatches 291;
                                        1.9e-44;
       Score 237.4;
                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
22.0%;
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                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        445 AGATC----
                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       868
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                                                                        Matches 462;
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          Query Match
                                           Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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cell growth; anti-ING1; CAb; isoform; diagnosis; tumour; antigen;
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Matches 462; Conservative
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                                                                                                                                           The invention discloses monoclonal antibodies which can be used, in combination, to specifically recognise epitopes of ING1 (inhibitor of growth 1) protein isoforms. ING1 is a tumour suppressor gene and its expression is regulated through the cell cycle, peaking in the S phase. Expression of ING1 is down regulated in breast tumours and lymphoid malignancies. Overexpression of a construct containing the ING1 gene is able to inhibit cell growth by reducing the fraction of cells which enter into the S phase. The monoclonal antibodies are useful for detecting an ING1 protein in a cell, which involves selecting a cell that ectopically or endogenously expresses ING1 protein. The anti-ING1 monoclonal antibody combination consists of two or more antibodies of CAbl-CAbl (not defined), preferably a mixture of CAbl-CAbd, which can detect at least two different isoforms of ING1. The antibodies are also useful for diagnosing a disease e.g. tumour or medical condition in an animal ansociated with abscrant levels of an ING1 protein. The sequence presented is the human inhibitor of growth I (ING1) isoform, and unman cDNA, library, which encodes a
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                                                Novel monoclonal antibody which specifically recognizes epitope of ING1, inhibitor of growth 1 protein, and designated CAb1-10, useful for detecting two different isoforms of ING1 and diagnosing a medical
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Pred. No. 6.1e-44;
0; Mismatches 290;
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Mutations in or loss of the p53 gene occur in more than 50% of human tumours and tumour cell lines, but functional inactivation of the p53 pathway occurs in a much larger proportion of tumours. In many cases the mechanism of functional inactivation of the p53 gene remains unknown but p53 has been found to act in cooperation with ING1. Functional cooperation between ING1 and p53 suggested that ING3 necoded a tumour suppressor protein that functioned within the p53 pathway. This data suggested a possible role for ING1 in head p53 pathway. This data suggested a possible role for ING1 in head can neck cancers and chromosomal location of the ING1 placed it within a region that is frequently rearranged in head and neck cancers. Large scale analysis of tumours involving ING1 has not cancers. Large scale analysis of tumours involving ING1 has not expression suggesting that ING1 was not a useful gene to study in cancer etiology. However, alternative initiation exons of the ing1 gene, each having their own promoter have been discovered.

Expression of one promoter (1a) produces a protein having ING1. Expression of a second promoter (1b) produces a protein having
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53; tumour; cancer; detection; antibody; hybridisation; exon 1b;
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AAH28479 standard; DNA; 1143

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an identical C-terminal fragment to ING1 but an additional 104
N-terminal amino acide. The newly discovered protein has been designated p37ING1 (Wild type: p33ING1). p37ING1 has the characteristics of an oncogene. When overexpressed in cells (even those expressing wild type p53) p37ING1 is able to cause proliferation or transformation of those cells. Thus detecting a nucleic acid encoding exon lb of ing1 by hybridisation with an inclear acid having the sequence of exon lb of ing1 by conceptual expressing the or its antisense sequence can identify individuals expressing the oncogenic form of ing1. Novel peptide sequences taken from the 104 or terminal peptide of p37ING1 can also be used to raise antibodies that can also be used in detection methods for the p37ING1 variant. The polypeptides may be useful in gene therapy for treatment of cell proliferation disorders, especially cancers and for diagnosing and
                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                                                                                                                                                                                                                                                                                    306 AACGTCTACAGCAGCTTCTCCAGAGGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGT
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                                                                                                                                                                                                                                                                                                                                DB 21; Length 1835;
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                                                                                                                                                                                                                                                                                            Sequence 1835 BP; 541 A; 387 C; 468 G; 439 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACACTCACAGTGTTTCCAAGATCCTGCTGAAA-----
                                                                                                                                                                                                                                                                                                                              Score 197.2; DB 21;
Pred. No. 3.7e-35;
0; Mismatches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            688
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 58.5%;
Matches 399; Conservative
                                                                                                                                                                                                                                                         studying cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a human cancer associated antigen. The sequence is the wildtype of the ING1 gene, which is a tumour suppressor gene candidate. The cancer associated antigen polynucleotides and polypeptides are useful for screening for the possible presence of a pathological condition in a subject such as cancer. The cancer associated antigen polypeptides are useful for producing vaccines.
                                                                                                                 Cancer associated antigen; ING1; tumour suppressor; cancer; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 CGCAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGCAGCCAGGAGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AAGAAACGTTAAAGGAAATTGATGATGTCTACGAAAAATATAAGAAAAAGAAGATGATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 GCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGCACGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated cancer associated nucleic acid molecule identified by SERE; (serological identification of antigens by recombinant expression cloning) technique, useful in nucleic acid based therapies to treat
                                                                                                                                                                                                                                      Ala)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1143;
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                                                                                                                                                                                                                    /transl_except= "(pos: 25..30, aa: Cys)"
/transl_except= "(pos: 124..126, aa: Pro,
/poroduct= "cancer asscociated antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gure
                                                                                    Nucleotide sequence of a human cancer associated antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1143 BP; 289 A; 291 C; 366 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            old L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 AAATGGAGTTACACTCACAGTGTTTCCAAGATC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Knuth A,
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                                                                                                                                                                            cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scanlan M,
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57.0%;
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24-OCT-2000; 2000US-0602362
                                                          (first entry)
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Best Local Similarity
Matches 394; Conserv
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P-PSDB; AAB84697.
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RESULT 13 AAH28479

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A partial cDNA clone (AAT69651), designated ING1, codes for a novel tumour suppressor protein p331NG1 (AAM19118) that is a potent inhibitor of cell growth. It was isolated by subtractive bybridisation between normal mammary and transformed epithelial cDNAs, isolation of an antisense ING1 cDNA insert that caused increased call profileration, and use of the insert that caused normal human fibroblast and Hela cDNA libraries. A complete ING1 sequence (AAT69652) was obtd. by 5'RACE. ING1 is localised to the 1943-34 chromosome region, to which a number of human cancers have been mapped. ING1 nucleic acids can be used in the diagnosis of breast cancer; a decreased level of ING1 mRNA indicates cancerous cells. They can also be used in gene therapy methods to block the
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Seguence 1902 BP; 574 A; 391 C; 461 G; 476 T; 0 other;
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                                                                                                                                        Query Match
Best Local Similarity 57.0%;
Matches 394; Conservative
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Location/Qualifiers 109..741 /\*tag= a

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gene; p331NG1; human; apoptosis; cell death; breast cancer;
                        brain tumour; gene therapy; tumour suppressor; ss
               Partial INGI partial cDNA sequence.
         18-JAN-1999 (first entry)
                                                 WO9844102-A2
                               Homo sapiens
                                                             26-MAR-1998;
                                                                   27-MAR-1997;
                                                      08-OCT-1998
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Modulating eukaryotic apoptosis by increasing p33ING1 activity -using p33ING1 derivatives, to induce apoptosis in cancer cells, and in the investigation of apoptotic pathways Following passage through a packaging line, normal mouse mammary spitherial cells were infected, and infected cells were injected into nude mice. Putative transforming fragments from tumours were isolated by PCR (see AAV62290-91) and subcloned into LNCX. An ING1 fragment was obtained and used to screen normal human fibroblast and HeLa cell CDNA libraries. 2. Clones were sequenced to obtain the partial ING1 sequence. The complete CDNA sequence (see This is the nucleotide sequence of a human ING1 (INhibitor of Growth) partial cDNA clone that codes for a pl33ING1 polypeptide (see AAM79674), a novel inhibitor of cell growth and a candidate tumour suppressor. ING1 is a new gene that is expressed in normal mammary epithelial cells, but which is expressed only at lower levels in several cancerous mammary epithelial cell lines and is not expressed in many primary brain tumours. To isolate ING1, a subtractive hybridisation of breast cancer cell line cDNAs was performed with cDNA from normal mammary epithelial cells, and subtracted cDNAs were cloned into retrovirus vector pLNCX. involves administering an antisense oligonuclectide. Also claimed are a method for determining the apoptotic characteristics of a eukaryotic cell, an assay for determining the level of p33ING1 activity in a eukaryotic cell, and an isolated eukaryotic cell substantially free of p33ING1 biological activity. The invention discloses ING1 derivatives or variants that may be used to induce apoptosis in eukaryotic cancer cells. AAV62292) was obtained by RACE. A claimed method to potentiate apoptosis in a eukaryotic cell involves administering an active p33ING1 peptide or an oligonucleotide encoding such as a peptide. A claimed method for inhibiting apoptosis in a eukaryotic cell Johnston RN, Riabowol K; (UYTE-) UNIV TECHNOLOGIES INT INC. Example 2; Fig 2; 66pp; English 98WO-CA00277 Helbing CC, WPI; 1998-542700/46. P-PSDB; AAW79674 Garkavtsev I,

Sequence 1902 BP; 574 A; 390 C; 462 G; 476 T; 0 other;

686 357 GAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGAC 416 508 509 TCTTCAAGAA--GACCCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGG 566 515 TCGACCCCAACGAACCCACGTACTGTCTGTGCAACCAGGTCTCCTATGGGGGAGATGATCG 574 GATGTGACAATGAACAGTGTCCAATTGAATGGTTTCACTTTTCATGTGTTTCACTTACCT 806 807 ATAAACCAAAGGGGAAATGGTATTGCCCCAAAGTGCAGGGGAGATAATGAGAAAAAAATGG 866 155 GCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGGAACCGCACGCGGC 214 215 AGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGGTGGGCGACACAGTGGGCA 274 275 ACAGCGGCAAGGTTGGCGCGGACAGGCCCAATGGCGATGCGGTAGCGCAGTCTGACAAGC 334 455 agaagaagaagcgcrccaaggccaaggcgaggcgaggggcgrcccrgccgagccrccca 514 95 CGCÁGAAGCGGCGGATGCTGCTGTGTGCAGCGCGCGCTGATCCGCAGCCAGGAGCTGG 154 450 -CTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGA AGAAAAAGAAACGCTCCAAGGCCAAGCAGGAAAGGGAAGCTTCACCTGTTGAGTTTGCAA TAGATCCTAATGAACCTACATACTGCTTATGCAACCAAGTGTCTTATGGGGAGATGATAG 867 ACAAAGTACTGAAAAGACAAAAAAGGATAG 897 695 ACAAAGCCCTGGAGAAATCCAAAAAAAGAGAG 725 687 747 627 셤 셤 g ద g ò 움 셤 ઠે 셤 8 원 ò d ð 8 ઠ ò 8

Search completed: January 12, 2004, 16:44:42 Job time : 344 secs

Matches 394; Conservative

Query Match Best Local Similarity

0; Mismatches 267; Indels 30; Gaps

Pred. No. 4.3e-32;

17.0%; Score 183.8; 57.0%; Pred. No. 4.3

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Run on:	January 12, 2004, 16:38:42; Search time 3978 Seconds (without alignments) 11106.686 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-513-365A-2 1080 1 gcggccgcggcggtgcatgaaaaaaaaaaaaaaa
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 segs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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AX211560 Sequence 7 from Patent W00159114. AX211560.1 GI:15523814	Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Harris, C.C. and Nagashima, M. Tumour suppressor gene, p47ing3 Patent: WO 0159114-A 7 16-AUG-2001;
RESULT 1 AX211560 LOCUS DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

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Nagashima, M., Shiseki, M., Miura, K., Hagiwara, K., Linke, S.P., Pedeux, R., Wang, X.W., Yokota, J., Riabowol, K. and Harris, C.C. DNA damage-inducible gene p331NG2 negatively regulates cell proliferation through acetylation of p53
Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9671-9676 (2001)
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Submitted (12-MAR-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, 37 Convent Drive Bldg.37 Rm.2C01,
Bethesda, MD 20892, USA
Location/Qualifiers
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RDLCHWANGTBDCDDQPREKKSKAKKKRSKAKQRREASPVEFAIDPNEPYCLCN
QVSYGEMIGCDNEQCPIEWFHFSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKO
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/translation="MLGQQQQQLYSSAALLIGERSRLLICYVQDYLECVESLPHDMQR
          PRI 20-MAY-2002
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Contact: nisc_mgc@nhgri.nih.gov
Akhter_N., Ayele.k., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighl,P.,
Hansen,N., Ho.S.-L., Karlins,B., Laric,P., Legaspi,R., Maduro,Q.L.,
Masslello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.,
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be four through the I.M.A.G.B. Consortium/LiML at: http://image.llnl.gov Series: IRAL Plate: 15 Row: m Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504694. Location/Qualifiers
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                                                                                                                                                                                                                     Strausberg, R. Direct Submission Submission Submitted (07-MAY-2002) National Institutes of Health, Mammalian Submitted (07-MAY-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   member 1-like, clone
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                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Gaithersburg, Maryland;
                                                                                                                                                                Craniata; Vertebrata; Butele
Catarrhini; Hominidae; Homo.
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/clone lib="NHH MGC 7"
/clone hort-inunom n"
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MGC:10524 IMAGE:3941655, mRNA, complete cds.
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Best Local Similarity 100.0%; Pred. No. 3.8e-220;
Matches 1073; Conservative 0; Mismatches 0;
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/mol_type="mRNA"
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        mRNA
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inhibitor of grown E:394167
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Mammalia, Eutheria, Primates,
1 (bases 1 to 1141)
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      GCGGCCGCGCCGGTGCATGTGCGCTGCTGGATGCGGAGGCGGCGGCGACGCGCGGAT
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                                                                                                                     GGAGCGGAGCCGGCTGCTCCTGCTACGTGCAGGACTACCTTGAGTGCGTGGAGTCGCT
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69 GCGCCGCGCCGCTGCTGCTGCTGGATGCGGAGGCGGCGCGCGC	301 GAAGAAACGTCTACAGAGCTTCTCCAGAGAGCACTAATTAAT	429 IGANTARATACACTCACAGTTTTCCAAGATCCTCGAAAGTGGAAGGTCGGGCCTCAG	481 AAAGATGGATTCCAGCCAACCAGAAAGATCTTCAAGAAGACCCGGAGGCAGCGGACCAG 540 	541 TGAAAGCCGTGATTTATGTCACATGGCAAATGGAGATTGAAGACTGTGATGATCAGCCACC 600 	601 TAAAGAAAATCCAAGTCAGCAAAGAAAAAAAAGCCTCCAAGGCCAAGCAGGAAAG 660 	661 GGAAGCTTCACCTGTTGAGTTTGCAATACATCCTAATGAACCTACATACTGCTTATGCAA 720 	721 CCAAGTGTCTTATGGGGAGATGATGACAATGAACAGTGTCCAATTGAATGGTT 780 	781 TCACTTTTCATGTGTTTCACTTACCTATAACCAAAGGGGAAATGGTATTGCCCAAAGTG 840 	841 CAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAGACAAAAAAGGATAGAAG 900 	901 ATCGAGGTAGTAAAGGCCATCCACATTTTAAAGGGTTATTGTCTTTTATATAATTCGTT 960	961 TGCTTTCAGAAAATGTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTA 1020 	1021 GTATTAATGGTGTATTAAAAGTTGTTGTACTTTGAAAAAAAA	RESULT 4 AR213555
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                               Length 1078;
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                          Score 1046; DB 9;
Pred. No. 2.4e-214;
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ilarity 99.5%;
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NVSVLRELDNKYQETLKEIDDYYEKYKKEDDLNQKKRLQQLLQRALINSQELGDEKIQ
TYQMLELPURPRARQMELHSQCFQDPAESERABARAKUDSQPERSSRRRPRQFTSES
RDLCHWANGIBCDDOPPERKKGSXKKKKRSRAKQREBASPVEFAIDPNEFYCLCN
QVSYGEMIGCDNEQCPIEWFHPSCVSLTYKPKGKWYCPKCGDNEKTMMKSTEKTYKD
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Catarrhini, Hominidae, Homo.
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Shimada, Y., Saito, A. and Horie, M.
Shimada, Y., Saito, A. and Horie, M.
Subrict Submission
Submisted (07-APR-1998) Yoshikazu Shimada, Otsuka Pharmaceutical
Co. Ltd., Otsuka GEN Research Institute; Kagasuno, Kawauchi-cho,
Tokushima, Tokushima 771-0192, Japan
(5-mail:shim@otsuka.genome.ad.jp, Tel:81-886-65-2888(ex.2476),
Sequence updated (17-Apr-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimada,Y., Saito,A., Suzuki,M., Takahashi,E. and Horie,M.
Cloning of a novel gene (ING1L) homologous to ING1, a candidate
                         CAGGGGAGATAATGAGAAAAAATACGACAAAAGTACTGAAAAAGACAAAAAAGGATAGAAG
                                                                                                                                                TGCTTTCAGAAAATGTTTTAGGGTAAATGCATAAGACTATGCAATAATTTTTAATCATTA
                                                                     CAGGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGGACAAAAAGGATAGAAG
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/dev_stage="fetal"
/tissue_lib="fetal-brain"
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/db_xref="GI:4115555"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="4"
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/codon_start=1
/product="ING1Lp"
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 ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTA
                                                  CACTCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATG
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Location/Qualifiers
1. 840
/organism="unknown"
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NVSVLRELDNKYQETLKEIDDYYEKYKKEDDLMQKKRLQQLLQRALINSQELGDEKIQ
YOYULLELVBNRARQMELHAGOFQDPRESERASDKAKMDSSQPERSSRRPRQRTSES
RDLCHWANGTEDCDQOPPERKSSKAKKKRSKAKQEREASVWEFAIDPNBFTYCLCN
QVSYGEMIGCDNEQCPIEWFHPSCVSLTYKPKGKWYCPKCRGDNEKTMDKSTEKTKKD
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                                                                                            PRI 06-JAN-2001
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Submitted (08-JUN-1998) Lopez-Otin C., Bioquimica y Biologia
Molecular, Universidad de Oviedo. Facultad de Medicina., C/ Julian
Claveria s/n., 33006, SPAIN
Location/Qualifiers
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Pred. No. 4.8e-170;
0; Mismatches 2;
               GTATTAATGGTGTATTAAAAGTTGTTGTACTTTG 1054
                                                                                                                                                                                                                           Cal,S., Freije,J.M. and Lopez-Otin,C.
MTG2, a new possible gene supressor tumor
Unpublished
2 (bases 1 to 843)
                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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1. .843
/gene="ing2"
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                                                                                      Homo sapiens mRNA for p32 protein.
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/gene="ing2"
/codon_start=1
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il Similarity 99.8%;
841; Conservative
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Homo sapiens (human)
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Mammalia; Eutheria;
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188   GACATGCAGAGGAACTTCTTCTCTCCGGAGGCTCGAGGAACTTCTACACAAAACTTCTCAGAAAACTTCTTCAGAAAACTTCTACACAAAAACTTCTACACAAAAACTTCAGAAAACTTCAGAAAAATTTCAGAAAATTTCAGAAAATTTCAGAAAATTTCAGAAAATTTCAGAAAATTTCAGAAAATTTCAGAAAATTTCAGAAATTCAGAAAAAAAA	TA 247 Qy 211 GCTGCGAGAGCTGGACAACAATATCAAGAAACGTTAAAGGAAATTGATGATGATGTCTACGA 270	AB 307 QY 271 AAAATATAAGAAAGATGATTTAAACCAGAAGAAACGTCTACAGCAGCTTCTCCAGAG 330	AA 367 OY 331 AGCACTAATTAATAGTCAAGAATTGGGGGGGTGAAAAAATACAGATTGTTACACAAATGCT 390	427 Qy 391 CGAATTGGTGGAAAATCGGGCAAGACAAATGGAGTTACACTCACAGGTGTTTCCAAGATCG	TG 487 Qy 451 TGCTGAAAGTGAACGAGCCTCAGATAAAGCAAAGATGGATTCCAGCCAACCAGAAAGATC 510	Qy 511 TTCAAGAAGACCCGCAGGCAGCGGACCAGTGAAAGCCGTGATTTATGTCACATGGCAAA 570	AA         607         571         TGGGATTGAAGACTGTGATGATCAGCCACCTAAAGAAAGA	CT 667 Qy 631 AAAGAAACGCTCCAAGGCAAGAAAGGAAAGGTTCACCTGTTGAATTAGA 690	TG 727 Qy 691 TCCTAATGAACCTACATACTGCTTATGCAAGTGTCTTATGGGGAGATGATGATGATG 750	TT 787 QY 751 TGACAATGAACAGTGTCCAATTGAATGGTTTTCACTTTTCACTTTTCACTTTACCTATAR 810   1	GA 847         QY         811 ACCAAAGGGAAATGGTATTGCCCAAAGGGGAGATAATGAGAAAACAATGGACAA 870	Qy   871 AAGTACTGAAAAGATAGGATAGAGATGAGGTAGTAAAGGCCATCCACATTTTA 930		Oy 1051 TTTGAAAAAAAA 1064 Db 1141 TTTGAAAAAAAA 1154	SULT 9 ING3S2 CUS CUS FINITION Homo sapiens p33 (IN COMplete cds.	
										H-H	E+E+		AR220840 1154 bp DNA linear PAT 26- NN Sequence 81 from patent US 6426186. 1 AR220840 GI:23327717	SM	1 (bases 1 to 1154) Jones, K. A., Volkmuth, W. and Walker, M.G. Bone remodeline, Bones Patent: US 6426186-A 81 30-JUL-2002; Location/Qualifiers e / organism="unknown" 367 a 216 c 285 g 265 t 21 other	Action Materials of the Control of t

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AC107214 15-OCT-2002
Homo sapiens BAC clone RP11-367N14 from 4, complete sequence.
AC107214
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Louis,
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                                                                                                                                                                                                                       Craniata, Vertebrata, Euteleostomi;
Catarrhini, Hominidae, Homo.
                              TTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAATGAACAATT
                                                                                                                                                            GAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGC
                                                                                                                                                                                                      CCAAAGTGCAGGGGAGATAATGAGAAACAATGGACAAAAGTACTGAAAAAGACAAAAAG
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                                                                           TTATGCAACCAAGTGTCTTATGGGGAGATGATAGGATGTGACAATGAACAGTGTCCAATT
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4444 Forest Park Parkway,
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Nguyen,C., Haglund,K. and Spalding,L.

The sequence of Homo sapiens BAC clone RP11-367N14

Upublished (2001)

3 (bases 1 to 183317)
                                                                                                                                                                                                                                                                                                                                                                                           AATCATTAGTATTAATGGTGTATTAAAAGTTGTTGTACTTTG 1054
                                                                                                                                                                                                                                                                                                                                                                                                            Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Mammalia, Eutheria, Primates;
1 (bases 1 to 18317)
Sulston, J.E. and Waterston, R.
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4 (bases 1 to 183317)
Waterston, R.H.
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6 (bases 1 to 183317)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 974)
Nagaabima, M., Hagiwara, K., Minter, A.R. and Harris, C.C.
Direct Submission
Direct Submission
National Cancer Institute, 37 Convent Dr. Bidg. 37, Rm. 2C26, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGACAAATGGAGTTACACTCCACAGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCA
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|product="p33 ING2"
|oin(AF062747.1:68. .239,124. .794)
                                                                                                                                                                                                                       'gene="ING2"
join(AF062747.1:1. .239,124. .938)
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Pred. No. 3.6e-165;
0; Mismatches 3;
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                                                                      Submitted (15-OCT-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 20, 2002 this sequence version replaced gi:20128734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA 7 (bases 1 to 183317)
                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this form. I may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC112698.
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                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted:
                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Data from AC112698 was used to finish this clone
                                                                                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                            Center project name: H_NH0367N14
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856. 1214
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/rpt family="MaLR"
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                                                                                                                                                                                                                           Mus musculus
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Butaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1001)
Nagashima,M., Hagiwara,K., Hancock,A.R. and Harris,C.C.
Direct Submission
Submitted (16-7UL-1998) Laboratory of Human Carcinogenesis,
National Cancer Institute, National Institutes of Health, 37
Convent Dr., Bldg. 37, Rm. 2C01, Bethesda, MD 20892, USA
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Mus musculus p331NG2 (Ing2) mRNA, complete cds.
AF078834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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1. 1001
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Best Local Similarity 88.1%;
Matches 887; Conservative
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                                                                                                                                                                                                                                                                                                                              Score 817.2; DB 9;
Pred. No. 1.1e-164;
0; Mismatches 3;
                                                                                                                                                                                                                                                     23182. .23212
/rpt_family="(TAAA)n"
                                                                                                                                                                                             /rpt_family="Alu"
/rpt_family="Alu"
/23182, 23182
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22072. 22381
/rpt_family="Alu"
22432. 22526
/rpt_family="MIR"
23055. 23181
  /rpt_family="Alu"
21605. .21740
/rpt_family="Alu"
21746. .22060
family="Alu"
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Best Local Similarity 99.6%;
Matches 819; Conservative
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/translation="MLGQQQQQLYSSAALLTGERSRLLTCYVQDYLECVESLPHDMQ
RNVSYLRELDNKYQETLKEIDDYZRKYKKEDDSNQKKRLQOHLQRALINSQELGDEKI
QTTQMLELVENRARQWELHSQCCQDAESERASDKSKMSSSQPERSSRRPRRQRTSE
SRDLCHWTNGIDDCDQPPKEKRSKAKKKKRSKAKQERAQDERASPUERILDPNEPTYCLC
NQVSYGEMIGCDNEQCPIEWPHSCVSLTYKPKGKWYCPKCRGDNEXTWDKSTEKTKK
Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McClowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J. W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 108 Row. o Column: 20 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 12963706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGTTAAAGGAAATTGATGATGTCTACGAAAAATATAAGAAGAAGATGATTTAAACCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="Similar to inhibitor of growth family, member
1-like"
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Pred. No. 5.3e-140;
0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:6515125"
/tissue type="Mammary tumor. Mmold mouse. Taken by biopsy."
/clone lib="NCI CGAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAH50003.1"
/db_xref="GI:29436710"
                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
                                                                                                                                                                                                                                           Location/Qualifiers
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Matches 78(
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 1262)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
                      GTCGAAGATGGATTCCAGTCAACCGGAAAGATCTTCTAGAAGACCTCGAAGACAGAGAC
                                                                                                                                                                                    TAACCAAGTGTCCTACGGGGAGATGATAGGCTGTGACAATGAACAGTGTCCCATTGAATG
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CAGTGAAAGCCGTGATTTATGTCACATGGCAAATGGGATTGAAGACTGTGATGATCAGCC
                                                                                                    CAGTGAGAGCCGTGACTTATGTCACATGACAACGGGATTGACGACTGTGATGATGATCAACC
                                                                                                                                                           AAGGGAAGCTTCACCTGTTGAGTTTGCAATAGATCCTAATGAACCTACATACTGCTTATG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Submitted (31-MAR-2003) National Institutes of
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                          841 GAAGATGCAGTCAACCGGAAAGATCTTCTAGAAGACCTCGAAGACAGAGACAGA
                                                                                                                                                                                541 TGAAAGCCGTGATTTATGTCACATGGCAATGGGATTGAAGACTGTGATGATCAGCCACC
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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Rattus norvegicus
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Submitted (05-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Say Genome Sequencing Consortium.

S. Rat Genome Sequencing Consortium.

AL Direct Submission

Direct Submission

Nov-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23264819.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and whole sequence contigs are confered and oriented, and separated in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                 Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Kar, M., Mahmoud, M., Malloy, K., Marchin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mandariet, M., Mahney, S., McLeedd, M.P., McNeil, T. Z., Menen, E., Milosavljevic, A., Miner, G., Minia, E., Montemayor, J., Moore, S., Minias, E., Montemayor, J., Moore, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Murphy, M., Nair, L., Nankeris, S., Nankeris, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, M., Ren, Y., Reuter, M., Richards, S., Parks, K., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Ouiroz, J., Rachlin, E., Reves, K., Regier, M., Saker, S., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvattsbeyn, A., Stsson, I., Sitter, C. D., Smajs, D., Shetty, J., Shvattsbeyn, A., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wang, S., Warten, J., Walker, M., Trejos, Z., Usmani, K., Valas, R., Weight, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Williams, G. and Gibbs, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R., Smith, D.R., Holt, R., Smith, D. Prizer, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Center code: BCM
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 231311;
                                                                                                                                                                                 22535 225734: gap of unknown length 22535 225734: gap of unknown length 225735 231311: contig of 5577 bp in length. Location/Qualifiers 1.23131 | forgation=Rattus norvegicus" | /organism="Rattus norvegicus" | /db_xref="taxon:10116" | /dlo_xref="taxon:10116" | /dlo_xref="taxon:10116" | /dlo_xref="taxon:10116" | /dlo_xref="taxon:10116" | /dlo_xref="taxon:10116" | /dlo_xref="taxon:10124" | /dlo_xref="taxon:10116" | /dlo_xref="taxon:1
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Pred. No. 1.3e-136;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end_sequence:BH343917"
complement(218103, .218757)
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:BH343918"
220260. .222134
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222185. .225634
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Best Local Similarity 90.5%;
Matches 744; Conservative 0
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1 (Dages 1 to 249104)

1 (Dages 2 to 249104)

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Rattus norvegicus clone CH230-129P3, WORKING DRAFT SEQUENCE, 3
unordered pieces.
    832
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Rodentia, Sciurognathi, Muridae, Murinae,
                                                   52756 GAGTGGTTTCACTTTTCCTGCGTTTCACTCACCTATAAACCAAAGGGGAAATGGTATTGC
                                                                                                                                                                                  CCAAAGTGCAGGGAGATAATGAGAAAACAATGGACAAAAGTACTGAAAAAGACAAAAAAG
                                                                                                                                                                                                                                      52696 CCAAAGTGCAGGGAGACAGTGAGAAAACCATGGACAAAAAGTACTGAAAAAAGGAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52636 GAGAGAAGAGCGAGGTAGTGAAGGCCATCC-GGTTTTAAAGGGGTTCTTTGTCTTTTATAT
773 GAATGGTTTCACTTTTCATGTGTTTCACTTACCTATAAACCAAAGGGGAAATGGTATTGC
                                                                                                                                                                                                                                                                                                                                                                GATAGAAGATCGAGGTAGTAAAAGGCCATCCACATTTTAAAGGGTTATTTGTCTTTTATAT
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HTG; HTGS PHASEI; HTGS DRAFT; I
Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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'db xref="taxon:10116"
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                                                                             1. .1042
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Matches 744; Conserv
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MORIECT SUBMISSION

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DIRECT SUBMISSION

ALC SUBMISSION

MORICCULAR AND HUMAN GENOME SEQUENCING CENTER, DEPARTMENT OF MORICCULAR HOUSEON, TX 77030, USA

SUBMISSION

CES 3 (DASSES I to 245104)

RAT GENOME SEQUENCING CONSORTIUM.

DIRECT SUBMISSION

ALC SUBMISSION

NOVE 150202 HUMAN GENOME SEQUENCING CENTER, DEPARTMENT OF MORICCULAR AND HUMAN GENOME SEQUENCING OF MORICCULAR AND HUMAN GENOME SEQUENCING OF MORICCULAR AND HUMAN GENOME SEQUENCE OF MORICCULAR AND HUMAN TO 70030, USA

ON NOV 15, 2002 this sequence version replaced gi:23265010.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Esch contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Waldron, L., Walker, B., Wang, J., Willsams, G., Willson, R., Weber, M., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weise, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center clone name: GTA30-129P3
Center clone name: CTA30-129P3
Consensus quality: 202567 bases at least Q40
Consensus quality: 204753 bases at least Q30
Consensus quality: 205947 bases at least Q30
Consensus quality: 205944 bases at least Q30
Consensus quality: 205947 bases at least Q30
Consensus quality: 205947 bases at least Q30
Consensus quality: 205947 bases; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 TTGGGAGATGAAAAATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCA
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45075 c 46272 g 57482 t 38750 others
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Pred. No. 1.3e-136;
); Mismatches 77;
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240971. .241683
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                                                                                           clone_end:Sp6
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DEFINITION ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

AC094539/c

RESULT 15

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Direct Submission

L Submitted (109-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza. Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:24942175.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Arlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the facture table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated alse. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 247796)

Rat Genome Sequencing Consortium.
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1 247796: contig of 247796 bp in length.
Location/Qualifiers
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/note="wgs_contig"
68374 a 51336 c 52193 g 65763 t 10130 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: GAVT
Center clone name: CH230-419
-------- Summary Statistics
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/db_xref="taxon:10116"
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Milan,C., Malten, H., Alberbooks, S., Amin, A., Anguinano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Alberbooks, S., Amin, A., Anguinano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baladrin, D., Bandaranike, D., Barber M., Baca, E., Baden, H., Baladrin, D., Bandaranike, D., Barber M., Barnstead, M., Benahmed, F., Biswalo, K., Elyth, P., Barnstead, M., Benahmed, F., Biswalo, K., Carez, C., Cave, M., Cree, J., Coura, J., Chu, J., Charden, V., Carez, C., Burch, P., Burrell, K., Carden, C., Coyle, M., Cree, J., Divola, L., Davy-Carroll, L., De Anda, C., Dederich, D., Davyla, M., Leben, D., Dramon, S., Deramo, C., Coyle, M., Cree, J., Divola, K., Davyla, M., Lose, J., Divola, K., Davyla, M., Deramo, C., Ding, Y., Dinh, H., Divola, K., Davyla, M., Deramo, C., Ding, Y., Dinh, H., Divola, K., Davyla, M., Deramo, C., Ding, Y., Dinh, H., Divola, K., Drase, C., Deramo, C., Ding, Y., Dinh, H., Divola, K., Drase, C., Ding, Y., Dinh, H., Divola, K., Drase, C., Gola, M., Dural, B., Divola, M., Deteron, E., Fernandez, S., Finley, M., Rlaggi, N., Forbes, M., Garner, T., Garza, M., Guevara, W., Marlin, R., Mar
                                                                                                                                                                                                                                                                             DNA linear HTG 09-MAY-2003
*** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                         110358 AATCATTAGTATTGATGGTGTATTAAAAGTTGTTGTACTTTG 110317
                                                                                                                                                                                                                                                                                                                                                                      AC094539.6 GI:30466722
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                             AC094539 247796 bp
Rattus norvegicus clone CH230-419,
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Direct Submission
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1; Gaps

Indels

TITLE JOURNAL REFERENCE AUTHORS TITLE

Length 247796;

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216779 GACAAATCCAAGATGGATTCCAGTCAACCCGAAAGATTCCAGAAGACCTCGAAGACCTCGAAGACAG 216720
                                                                                                                                                                                                                                                                                                        216959 TCAAACCAGAAAAACGCCTACAGCAGCATCCTCCAGAGAGCATTAATCAATAGCCAAGAA 216900
                                                                                                   216660
                                                                                                                                                                                                                                                                              216659 CAGCCACCGAAAGAAAAAAATCCAAATCCGCCAAGAAGAAAAAGCGCTCCAAGGCCAAG 216600
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                                                                                   413 AGACAAATGGAGTTACACTCCACGTGTTTCCAAGATCCTGCTGAAAGTGAACGAGCCTCA 472
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	using frame plus p2n model	January 12, 2004, 19:31:18 ; Search (without		IILLE:     US-U9-513-365A-1 Perfect score: 1481 Sequence: 1 MLGQQQQQLXSSAALLTGERDNEKTWDKSTEKTKKDRRSR 280	10.0 , Xgapext	Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0	Searched: 2276164 segs, 1736306516 residues	Total number of hits satisfying chosen parameters: 4552328	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Command line parameters: -MODEL=frame+ p2n.model -DEV=xlp	-0=/cgn2 1/USPTO spool p/US09513365/runat 12012004 163934 28802/app query.fasta_1.455 -DB=Published Applications NA -QFWT=fastap -SUPFIX=p2n.rnpb -MINMATCH=0.1	-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100	-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0 -MAKLEN=2000000000 -USRE=G18095131356 GCGM 1 1 107 Grunnat 12012004 163914 28802 -MODIT-6 -ICPIT-3 -NO MMAP -INDEPROVEMENT - NO MMAP - NO MMAP -INDEPROVEMENT - NO MMAP - NO	-LONGLOG -DEV TIMEOTT-120 -WARN TIMEOTT-30 -THEREDS-1 -XGAPOP-10 -XGAPERT-0.5 -FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7	· ·	2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:* 3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:* 4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*	•• ••		. ㅇ ㄷ	0 m 5	15	<pre>17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:* 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	\$	Result Query No. Score Match Length DB ID Description

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     human embryonic brain cDNA library
                                      Conservative:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OSELUA Pharmaceutical Co., Ltd.
TILLE OF INVENTION: Human TSC403 gene and hum
FILE REFERENCE: 060193
CURRENT APPLICATION NUMBER: US/10/115,899
CURRENT APPLICATION NUMBER: 09/601,478
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 1998-04-26
PRIOR APPLICATION NUMBER: JP H10-134679
PRIOR FILING DATE: 1998-04-26
PRIOR FILING DATE: 1998-04-26
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PRIOR PLING DATE: 1998-02-03
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PRIOR PLING DATE: 1998-02-03
SOFTWARE: PATENTION NUMBER: JP H10-38133
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NAME/KEY: CDS
LOCATION: (92)..(931)
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ORGANISM: Homo sapiens
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202 CAGAAGCGGCGGATGCTGCACTGTGTGCAGCGCGCGCTGATCCGCAGCCAGGAGCTGGGC 261
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                                                                                                                                                               LeuProHisAspMetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGln 57
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18 GlyGluArgSerArgLeuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSer
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310 CTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACGCACG 369
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                  Riabowol, Karľ
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
Pathway
                                                                                                                                                                                         CUMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/968,653A

FILING DATE: 01-Oct-2001

CLASSIFICATION: AUKnown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/006,783A

FILING DATE: 15-JAN-1998

ATTORNY AGENT INFORMATION:

NAME: NO. US2003300/3084Alnan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET WUMBER: 35,303
                                                                                                         & Berghoff
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Matches:
Conservative:
Mismatches:
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                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert
STREET: 300 South Wacker Drive
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LOCATION: 16..897
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2061 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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722.00
74.36%
57.69%
                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                        NUMBER OF SEQUENCES:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 AsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSerLysSerAlaLys 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 SerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAla
 - refer to PALM or file wrapper
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Mismatches:
Indels:
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Prior application data removed NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3454
LENGTH: 8487
                                                                                                                                                                            7.72e-72
728.00
75.22$
59.13$
49.16$
                                                                                                        ; ORGANISM: Homo sapiens
US-09-764-877-3454
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US-09-968-653A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 ArgGlnArgThrSerGluSerArgAspLeuCysHisMetAlaAsnGlyIleGluAspCys 173
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                                                                                                                                                                                                                                                                                                          86 LeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLysIleGlnIleValThr
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Publication No. US20030073623A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                   633
125
29
36
14
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Conservative:
Mismatches:
Indels:
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S
                                     LOCATION: 1..630
SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                          244 SerieuThrTyriysProlysGlyLysTrpTyrCysProlysCysArgGlyAspAsnGlu
                 GlnProGluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAspLeu
                                     CysHisMetAlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSer
                                                                                                                         544 GCGTCCAGCAACCACGACCACGACGGCGCCTCGGGCACACCCAAGGAGAAGAAGGCC
                                                                                                                                                                     LysSerAlaLysLysLysLysArgSerLysAlaLysGInGluArgGluAlaSerProVal
                                                                                                                                                                                                                                                                                                                        GluMetileGlyCysAspAsnGluGlnCysProileGluTrpPheHisPheSerCysVal
                                                                                                                                                                                                                                                204 GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGlnValSerTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09968653A
Publication No. US20030073084A1
GENERAL INFORMATION:
APPLICANT: Gudkev, Andrey V
Garkavstev, Igor
Riabowol, Karl
TITLE OF INVENTION: p33/ING1 as a Mediator of p53 Signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 6606
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,653A
FILING DATE: 10-CCL-2001
CLASSIFICATION CHURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/006,783A
FILING DATE: 15-JAN-1998
ATTORNEY/AGDNT INFORMATION:
NAME: NO. USZ0030030844Anan, Kevin E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: 11linois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGACCATGGACAAAGCCCTGGAGAAATCCAAAAAAGAGAGG 885
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REFERENCE/DOCKET NUMBER: 97,837
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 633 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-968-653A-6
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Percent Similarity:
Best Local Similarity:
                                          Alignment Scores:
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                                                                                                                                           Query Match:
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APPLICANT: Asundi, Use
APPLICANT: Abandi, Use
APPLICANT: Chang, Use
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BCIP
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR PILING DATE: 2000-04-05
PRIOR PILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 37033 LENGTH: 421
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US-10-117-722-435
Sequence 435, Application US/10117722
Publication No. US20030219744A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                      Ö
                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (1).T.(421)
OTHER INFORMATION: n = A,T,C or
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474.00
90.00$
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; LOCATION: (164)..(1420)
US-10-117-722-435
                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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983 GGCTATTCATCATCTTCGGCACTTATGACAACATTAACACAGAATGCCAGTTCATCAGCA 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ------GATCAACTAGAACAAAGGTCAGTGAATTCTTTATGAATGCAAAGAAAAT 322
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                                                                                                                                                                                                                                              95 GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
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  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                Indels:
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1.03e-30
359.00
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983 GGCTATTCATCATCTTCGGCACTTATGACAACATTAACACAGAATGCCAGTTCATCAGCA 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 GluLeuGlyAspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArg 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetGlnArgAsnValSerValLeuArgGluLeuAspAsnLysTyrGlnGluThrLeuLys 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ArgleuGlnGlnLeu-----LeuGlnArgAlaLeuIleAsnSerGln 94
                                                                                                                                                                                                                                                                                                                                 ArgleuLeuThrCysTyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAsp
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                                      Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                256 ACGCGCAGGTGGACAGCCACGTGGAGCTGTTCGAGGCGCAGCAGGAGCTGGGCGAACAA 315
                                                                                                                                                                                                                                                       375
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115 AlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu---SerGluArg 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 LysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyrLysLysGluAsp 74
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                                                             196 GAGCTGGGCGACGAGAAGATCCAGATCGTGAGCCAGATGGTGGAGCTGGTGGAGAACCGC
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                                                                                                      GluLeuGlyAspGluLys1leGlnIleValThrGlnMetLeuGluLeuValGluAsnArg
                                                                                                                                                                                                                                                   AspleuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln
                                           AspleuAsnGlnLysLysArgLeuGlnGlnLeuLeuGlnArgAlaLeuIleAsnSerGln
                                                                                                                                                                                                                                                                                     146 ---GluargSerSerArgArgProArgArgGlnArgThrSerGluSerArgAsp 162
                                                                                                                                                                                                                                                                                                    376 GACAAGCCCAACAGCGAAGCGCTCACGGCGGCAGCAACAACGAGAACCGTGAG 429
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; Sequence 146, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNC
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SEQ ID NOS: 735
; SEQ ID NO 146
; FILE
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                                1103 TCATCTTCCTCCTCCTCTTCCTTATCATCGTGTTCTTCATCATCAACTGTTGTACAA 1162
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                                                               -SerProValGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 146, Application US/09738973

Sequence 146, Application US/09738973

Patent NO. US20020110563A1

GENERAL INFORMATION.

APPLICANT: Henderson, Robert A.

APPLICANT: Honderson, Robert A.

APPLICANT: Mohamath, Raodoh

APPLICANT: Bliot, Mark

APPLICANT: Ralos, Michael D.

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.475C9

CURRENT APPLICATION NUMBER: US/09/738,973

CURRENT FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 587

SOFTWARE: FARENCE FOR WINDORS SER
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      198 ArgGluAla-
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Best Local Similarity:
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Pred. No.:
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PLANTS CONTAINING

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111 ValGluAsnArgAlaArgGlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGlu 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TyrValGlnAspTyrLeuGluCysValGluSerLeuProHisAspMetGlnArgAsnVal 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 TAIGHTGATGATTACCTTGAGTAIGCAAGCACTTICCCTGCAGAGGTACAAGATTACTA 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54 ------AsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyrGluLysTyr 70
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                                                                                                                        APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLAN
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPISON BABER: US/09/938,842A
CURRENT APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
SPRIOR PILING DATE: 2001-01-16
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                                 Sequence 1178, Application
Patent No. US20020160378A1
GENERAL INFORMATION:
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          US-09-938-842A-1178
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                                                                                                                                            146 ---GluArgSerSerArgArgProArgArgGlnArgThrSerGluSerArgAsp 162
                                                                                                                                                                                                                                                                    376 GACAAGCCCAACAGCGCACCACGCGCAGCGCAACAACGAGAAACCGTGAG 429
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Sequence 146, Application US/1014649A

Publication No. US20030118599A1

GENERAL INFORMATION:

APPLICANT: Wang, Tongrong

APPLICANT: Fan, Liqun

APPLICANT: Algate, Paul A.

APPLICANT: Momell, Particia D.

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.475C11

CURRENT APPLICATION NUMBER: US/10/144,649A

CURRENT FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 749

SOFTWARE: FastESQ for Windows Version 3.0

SECTION 146
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Conservative:
Mismatches:
Indels:
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                                                                                             134 AlaSerAspLysAlaLysMetAspSerSerGlnPro-
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Best Local Similarity:
Query Match:
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US-10-144-649A-146
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Sequence 6348, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang
APPLICANT: Charles, Boone
APPLICANT: Howard, Bussey
TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
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310 TTAGAATTGGCGTATGAAGTCGCAATCAAGAACACAGAAATTCCTAGAGGTTTAAGACTG 369
                                                                                                                                                                                                                                                                                    430 AAATCAACAGCAAATCGTCGCAGGCACTGAAGAGCGAATCAAGAAGAAGCCATGGCT 489
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                                                                                                                                                                              ---HisSerGlnCysPheGlnAspProAlaGluSerGluArgAlaSerAsp 136
                                                                                                                                                                                                                370 GETGTGGACAACCATCCAGCAATGCACCTCCATCATGAACTAATGGAAAAATAGAGAGC 429
                                                                                                                                                                                                                                                                                                                         -----ArgThrSerGluSerArg 161
                                                                                                                                                                                                                                                                                                                                                                                                  AspLeuCysHisMetAlaAsnGlyIleGluAspCysAspAspAspGlnProProLysGluLys 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189 LysLysArgSerLysAlaLysGlnGluArgGluAlaSerProValGluPheAlaIle--- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  730 GTCAATAATGGCAGGATAGGTACATCTACAGCGTCCAGGGGAGTTAGCAGCGTCGGAAAC 789
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                                     AspGluLysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgGln 117
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                                                                      GAGGAGAAAATGCATGTCTCATCCATTATGCTGGATAATCTAGACAGATTGACGTCCCGG
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211 AATATCAACAAGATTTATGAAGAACTGATGCCATCGCTG-
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CURRENT APPLICATION NUMBER: US/10/032,585
CURRENT FILING DATE: 2001-12-20
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SOFTWARE: PatentIn version 3.1
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US-10-032-585-6348
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APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
ITILE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REPERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2010.1-03-07
PRIOR PPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 257
LENGTH: 993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 ValleuArgGluLeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspAspValTyr 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- CCAGGAAGCAATCGGAAAGACCT
                                                         200 aSerProVal---GluPheAlaIleAspProAsnGluProThrTyrCysLeuCysAsnGl
                                                                                           537 TATGCCAATTGAAGAGCAGCCAATCGATCCAAACGAACCAACTTACTGTGTCTGCCATCA
                                                                                                                              nValSerTyrGlyGluMetIleGlyCysAspAsnGluGlnCysPro---IleGluTrpPh
                                                                                                                                                                                                                       eHisPheSerCysValSerLeuThrTyrLysPro-----LysGlyLysTrp 253
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No. US20020128250Alman, Thea
                                                                                                                                                                                                                                                                                                           Sequence 257, Application US/09801368 Patent No. US20020128250A1
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US-09-801-368-257
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263.50
37.04%
23.15%
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Holtzman, Doug
Madden, Kevin
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Salama, Sofie
Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maxon, Mary
Milne, Todd
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Best Local Similarity:
Query Match:
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APPLICANT:
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US-10-032-	585-6348				,
Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	ment Scores: No.: :: Int Similarity: Local Similarity: . Match:	4.38e-19 253.00 25.58 25.388 17.088	Length: Matches: Conservative: Mismatches: Indels: Gaps:	897 84 36 108 104	
US-09-513-	365A-1 (1-28	0) x US-10-032-	585-6348 (1-897)		-
Oy Dp	19 GluArgSe ::: 4 GATACATC	erArgLeuLeuThrCysTyrValGlnAsp 	STyrValGlnAspTyrL	LeuGluCysValGluSerLeu ::: :::    TTATCTAATCTA	38 51
ò	39 ProHisAs	pMetGlnArgAsnVa	spMetGlnArgAsnValSerValLeuArgGluL	LeuAspAsnLysTyrGlnGlu	58
q	52 CCACTTGA	AGTGAGGCATTTATT	: AGAGGAAATCAAAAGC	 AAGATGTACAAGTCTC	111
λŏ	59 ThrLeuLy	6. —		GlulleAspAsp	65
qq	112 GCAAGGAAA	ACGATACCAAACTCG	TGACCATCAACTTCAT		171
<u>ک</u> و	66 ValTyrGluLy	uLysTyrLysLysGl	<b>4</b> =2	spaspLeuanGlnLysLysArgLeuGlnGlnLeu	85
ìè	1 4	121-01-1-1-07-05-0			4 0
	<b>4</b>	SALGREGIES ::: AGATATGAAGCTTGT	ATCGAAGAAGATATGAAGCTTGTGCAGAAACTACAGAAAGAGAAAAAAAA		273
'n	106 GlnMetLe	enGlufenValGluAs	euValGluAsnArgAlaArgGlnMet(	GlubeuHisSerGlnCysPhe	125
q <sub>0</sub>	274 ACTGCATT	 	 actgcattgtttttgatatcgaacatctatatcattttgag	 GAG	315
δò	126 GlnAspProAl	oAlaGluSerGluArgAl	æ	SerAspLysAlaLysMetAspSerSerGlnPro	145
qa	316		ACAGACATTGCC	AAGCTAGAAAGAGATGAATT-	347
ò	146 GluArgSe	erSerArgArgProAr	ProArgArgGlnArgThrSer	-GluSerArgAspLeuCysHi	165
q	348 GTTGCCTC	CTTTAGAACAC	TCGAGCTAACTGAAGT		407
ò	165 sMetAlaA	snGly11	ysAspAspGlnProPro	eGluAspCysAspAspGlnProProLysGluLysLysSerLysSe	185
q	408 ATCACTTA	ATGGCTTTTCTGATA	GTGCCTCTGCCACACC	CACTTAATGGCTTTTCTGATAGTGCCTCTGCCACACCAACGCCTAGGAATGGATCATC	467
ò	185 rala		Lys	LysLysLys	189
ΩD	468 ééchacte	CAGTGGCAGAAACAG	tgaaaagatccaaää	CTCCAGTGGCAGAACAGTGAAAAAGATCCAAAAGAAGAAACTTAGTGTTAAAGG	527
ò	190			LysArgSerLysAl	194
qq	528 GGCGTCCT	CTTCTCGCTCAGT	CATCCTCTGCTTCAAG	CGTCCTCTTCTGGCTCAGTCATCCTCTGCTTCAAGACAGGTGAAGCGACTCCGGTC	587
ò	194 aLysGlnG	sGlnGluArgGluAlaSerProVal	rovalGlu		204
qq	588 AGAAGAGA	TAGAGGATCCTCTAC	CGTATGAGGGAGGGTC	AGAAGAGATAGAGGATCCTCTACCGTATGAGGGAGGGTCATTGGCGTTCAATGGAAATGT	647
ò	205	PheAlaI	alleAspProAsnGluProThr	oThr	213
셤.	648 AGCAATGA	GCATAAATAGTGCAG	CAGATGCAAATGGTCC	TGAGCATAAATAGTGCAGCAGATGCTCCAAACGCCGAAGATGCTGATAA	707
δ	214T	YrCysLeuCysAsnG	lnValSerTyrGlyGl	TyrCygLeuCygAsnGlnValSerTyrGlyGluMetIleGlyCygAspAsnGl	231
qq	708 TAATCTAT	ATTGTTTTGTCAAC	GTGTTTCATTTGGTGA	AATGATTGGTTGTGATAATGA	797
ò 1	31	rolleGluTrpPheH	isPheSerCysValSe	uGlnCysProlleGluTrpPheHisPheSerCysValSerLeuThrTyrLysProLysGl	251
qq	89	AGTATGAATGGTTTC	ATTGGAGTTGTGTTGG	GATCACATCACCTCCTAAAGA	827
ò	251 уЬув	TrpTyrCysProL	ysCysArgGlyAspAsı	-TrpTyrCysProLysCysArgGlyAspAsnGluLysThrMetAspLysSe	269

Db	828 TGACGAAATTTGGTATTGTCCTGATTGTGCT
ò	269 rThrGlulysThrLysLysAspArgArgSer 279
Db	864 GATGGAGAAAAAAAAAGAAACGGAAGAAC 894
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